

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 28, 2004, 12:59:15 ; Search time 579 Seconds  
(without alignments)

2702.629 Million cell updates/sec

Title: US-10-017-084a-523

Perfect score: 2408

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Scoring table:

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Ygapop 1.0 , Ygapext 0.1  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2960401 seqs, 2274450654 residues

Total number of hits satisfying chosen parameters: 5920802

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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## ALIGNMENTS

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; Publication No. US20040038285A1  
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; APPLICANT: Ono Pharmaceutical Co., Ltd.  
; TITLE OF INVENTION: No. US20040038285A1el Polypeptides, cDNA encoding the same, and u  
; FILE REFERENCE: Q61459  
; CURRENT APPLICATION NUMBER: US/10/657,103  
; CURRENT FILING DATE: 2003-09-09  
; PRIOR FILING DATE: US/09/700,397  
; PRIOR FILING DATE: 2001-01-05  
; PRIOR APPLICATION NUMBER: JP 10-131815  
; PRIOR FILING DATE: 1998-05-14  
; PRIOR APPLICATION NUMBER: PCT/JP99/02485  
; PRIOR FILING DATE: 1999-05-13  
; NUMBER OF SEQ ID NOS: 19  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 1  
; LENGTH: 1032  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-657-103-1

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Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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## RESULT 2

US-09-978-295A-522  
; Sequence 522, Application US/09978295A  
; Patent No. US20020156006A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Daniel  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC11  
CURRENT APPLICATION NUMBER: US/09/978,295A  
CURRENT FILING DATE: 2001-10-15  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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US-10-017-084A-523 (1-344) x US-09-978-295A-522 (1-1679)

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Db 1154 CTTCTCAAAATTT 1165

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; Sequence 522, Application US/09978697
; Patent No. US20020169284A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
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APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE REFERENCE: P2630P1C27  
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US-10-017-084a-523 (1-344) x US-09-978-697-522 (1-1679)

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GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kijavini, Ivar J.

APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
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PRIOR APPLICATION NUMBER: 60/083500  
PRIOR FILING DATE: 1998-04-29  
PRIOR APPLICATION NUMBER: 60/083742  
PRIOR FILING DATE: 1998-04-30  
PRIOR APPLICATION NUMBER: 60/084366  
PRIOR FILING DATE: 1998-05-05  
PRIOR APPLICATION NUMBER: 60/084414  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084441  
PRIOR FILING DATE: 1998-05-06  
PRIOR APPLICATION NUMBER: 60/084637

1 PRIOR FILING DATE: 1998-05-07  
2 PRIOR APPLICATION NUMBER: 60/084639  
3 PRIOR FILING DATE: 1998-05-07  
4 PRIOR APPLICATION NUMBER: 60/084640  
5 PRIOR FILING DATE: 1998-05-07  
6 PRIOR APPLICATION NUMBER: 60/084598  
7 PRIOR FILING DATE: 1998-05-07  
8 PRIOR APPLICATION NUMBER: 60/084600  
9 PRIOR FILING DATE: 1998-05-07  
10 PRIOR APPLICATION NUMBER: 60/084627  
11 PRIOR FILING DATE: 1998-05-07  
12 PRIOR APPLICATION NUMBER: 60/084643  
13 PRIOR FILING DATE: 1998-05-07  
14 PRIOR APPLICATION NUMBER: 60/085339  
15 PRIOR FILING DATE: 1998-05-13  
16 PRIOR APPLICATION NUMBER: 60/085338  
17 PRIOR FILING DATE: 1998-05-13  
18 PRIOR APPLICATION NUMBER: 60/085323  
19 PRIOR FILING DATE: 1998-05-13  
20 PRIOR APPLICATION NUMBER: 60/085582  
21 PRIOR FILING DATE: 1998-05-15  
22 PRIOR APPLICATION NUMBER: 60/085700  
23 PRIOR FILING DATE: 1998-05-15  
24 PRIOR APPLICATION NUMBER: 60/085689  
25 PRIOR FILING DATE: 1998-05-15  
26 PRIOR APPLICATION NUMBER: 60/085579  
27 PRIOR FILING DATE: 1998-05-15  
28 PRIOR APPLICATION NUMBER: 60/085580  
29 PRIOR FILING DATE: 1998-05-15  
30 PRIOR APPLICATION NUMBER: 60/085573  
31 PRIOR FILING DATE: 1998-05-15  
32 PRIOR APPLICATION NUMBER: 60/085704  
33 PRIOR FILING DATE: 1998-05-15  
34 PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:  
Pred. No.: 1.19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-192A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTyrAlaIlePheThrGlyLeu 20  
DB 134 ATGAACCATCCAGCCAAATGCAATTTCTATCTTTGGCAATCTTCACGGGCTG 193  
QY 21 AlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
DB 194 GCTGCTCTGTCTCTCCAAAGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAA 253  
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
DB 254 GCTATGGAACAACGTGACGGTCCGGCAGGAGGAGCGCCACCATCTCTATGCTGGGATGAC 313  
QY 61 AsnArgValThrArgValAlaTyrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
DB 314 AACCGGGTCACCGGGTGCGCTGGCTTAACCGCAGCACCATCTCTATGCTGGGATGAC 373  
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
DB 374 AAGTGGTGCTGTGATCTCTCCGCTGGTCTTCTGAGCAACACCCCAACGCGAGTACGATC 433  
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
DB 434 GAGATCCAGAACGTGGATGTATGACGAGGGGCCCCCTTACACCTGCTCGGTCGAGACAGAC 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
DB 494 AACCCCAAGACCTTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553

QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
DB 554 ATTTCTTCAGATACTCCATTAATGAAGGAAACAATATTAGCTCCTCCTGATAGCACT 613  
QY 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180  
DB 614 GGTAGACCAGAGCCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673  
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
DB 674 AGTGAAGACGAATATCTTGAATAATCAGGGCATCACCCGGGAGCAGTCAAGGGGATAC 733  
QY 201 CysSerAlaSerAsnAspValAlaIleProValValArgValValValValValValVal 220  
DB 734 TGCAGTGGCTCCATGACGTGGCGCGCCGCTGGTACGAGAGTAAAGGTCAACGTGAAC 793  
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
DB 794 TATCCACCATACATTTCAAGAGCCAAAGGTACAGGTGTCCCGCTGGGACAAAAGGGGACA 853  
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260  
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCAGAGATTCAGAGATGACAAA 913  
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGAAACACACACTTTCTCTCAAACTC 973  
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGTGGCGCTCCCAACAG 1033  
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
DB 1034 CTGGGCCACACCATGCCAGCATCATGCTATTTGGTCAGGGCCCTGACGAGGTGAGC 1093  
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340  
DB 1094 AACGGCACGTGAGGAGGGCAGGCTGCTGGCTGGCTGCTTCTTCTGCTTGGCACCTG 1153  
QY 341 LeuLeuLysPhe 344  
DB 1154 CTTCTCAAAATTT 1165

RESULT 5  
US-09-999-832A-522  
; Sequence 522, Application US/09999832A  
; Publication No. US20020192706A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630P1G63  
CURRENT APPLICATION NUMBER: US/09/999,832A  
CURRENT FILING DATE: 2001-10-24  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
PRIOR FILING DATE: 1997-11-03  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066364  
PRIOR FILING DATE: 1997-11-21  
PRIOR APPLICATION NUMBER: 60/077450  
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PRIOR FILING DATE: 1998-05-07  
PRIOR APPLICATION NUMBER: 60/084598  
PRIOR FILING DATE: 1998-05-07

1 PRIOR APPLICATION NUMBER: 60/084600  
2 PRIOR FILING DATE: 1998-05-07  
3 PRIOR APPLICATION NUMBER: 60/084627  
4 PRIOR FILING DATE: 1998-05-07  
5 PRIOR APPLICATION NUMBER: 60/084643  
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7 PRIOR APPLICATION NUMBER: 60/085339  
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9 PRIOR APPLICATION NUMBER: 60/085338  
10 PRIOR FILING DATE: 1998-05-13  
11 PRIOR APPLICATION NUMBER: 60/085323  
12 PRIOR FILING DATE: 1998-05-13  
13 PRIOR APPLICATION NUMBER: 60/085582  
14 PRIOR FILING DATE: 1998-05-15  
15 PRIOR APPLICATION NUMBER: 60/085700  
16 PRIOR FILING DATE: 1998-05-15  
17 PRIOR APPLICATION NUMBER: 60/085689  
18 PRIOR FILING DATE: 1998-05-15  
19 PRIOR APPLICATION NUMBER: 60/085579  
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21 PRIOR APPLICATION NUMBER: 60/085580  
22 PRIOR FILING DATE: 1998-05-15  
23 PRIOR APPLICATION NUMBER: 60/085573  
24 PRIOR FILING DATE: 1998-05-15  
25 PRIOR APPLICATION NUMBER: 60/085704  
26 PRIOR FILING DATE: 1998-05-15  
27 PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 9 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-999-832A-522 (1-1679)

QY 1 MetiysThrleGlnProLysMetHisAsnSerleSerTrpAlallePheThrGlyLeu 20  
DB 134 ATGAAACCACTCCAGCCAAATATCTATCTCTTGGGCAATCTTTCAGGGGCTG 193  
QY 21 AlaAlaLeuCysLeuPheGlnGlyValproValArgSerGlyAspAlaThrPheProLys 40  
DB 194 GCTGCTGTGTCTTCTTCCAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253  
QY 41 AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp 60  
DB 254 GCTATGACACACGTGACGGTCCGCGAGGGGAGAGCGCCCTCAGGTGCATTTGAC 313  
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
DB 314 AACCGGTTCACCCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373  
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
DB 374 AAGTGGTGGCTTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGATC 433  
QY 101 GluileGlnAenValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
DB 434 GAGATCCAGACGCGGTGATGTATGACGAGGGCCCTTACACTGCTCGGTGCACAGAC 493  
QY 121 AsnHisProLysThrSerArgValHisLeuileValGlnValSerProLysIleValGlu 140  
DB 494 AACCAACCAAGAGCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553  
QY 141 IleSerSerApilleSerIleAsnGluGlyAsnAnilleSerLeuThrCysIleAlaThr 160  
DB 554 ATTCTCTCAGATATCTCCATTAATGAGGGAACCAATATTAGCCCTACCTCGATAGCACT 613  
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
DB 614 GGTAGACACGAGCTACGGTTACTTGGGAGACACATCTCTCCCAAGCGGTGGCTTGTG 673

QY 181 SerGluAspGluTyrLeuGluileGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
DB 674 AGTGAAGCAGATACCTTGAATTCAGGGCATCACCAGGAGCAGTCAGGGGACTACGAG 733  
QY 201 CysSerAlaSerAsnAspValAlaProValValArgArgValValValValValVal 220  
DB 734 TGCAGTGCCCTCCATGACGTGGCCCGCCGCTGGTGTACGAGAGTAAAGGTCCACCGTGAAC 793  
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
DB 794 TATCCACCATATCTTCAGAACCCAGGTGTCAGGTGTCCTCCGTCGAGCAAAAGGGGACA 853  
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleLysAspLys 260  
DB 854 CTGCACTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGGTACAGGATGACAAA 913  
QY 261 ArgLeuileGluGlyLysGlyValLysValGluAsnArgProPheLeuSerIleLeu 280  
DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973  
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
DB 974 ATCTTCTTCAATGCTCTCTGACATGACTATGGAACTACACTTGGTGGCTCCACAG 1033  
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
DB 1034 CTGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGGCCGCTCAGCGAGGTGAGC 1093  
QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340  
DB 1094 AACGGCACGTCCAGGAGGGGAGGCTCGTCTCGCTCGCTCTCTCTTCTTGTGTTCACCTG 1153  
QY 341 LeuLeuLysPhe 344  
DB 1154 CTCTCAAAATTT 1165

## RESULT 6

US-09-978-189-522  
; Sequence 522, Application US/09978189  
; Publication No. US20030004102A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C7  
; CURRENT APPLICATION NUMBER: US/09/978,189

1 CURRENT FILING DATE: 2001-10-15  
2 PRIOR APPLICATION NUMBER: 09/918585  
3 PRIOR FILING DATE: 2001-07-30  
4 PRIOR APPLICATION NUMBER: 60/062250  
5 PRIOR FILING DATE: 1997-10-17  
6 PRIOR APPLICATION NUMBER: 60/064249  
7 PRIOR FILING DATE: 1997-11-03  
8 PRIOR APPLICATION NUMBER: 60/065311  
9 PRIOR FILING DATE: 1997-11-13  
10 PRIOR APPLICATION NUMBER: 60/066364  
11 PRIOR FILING DATE: 1997-11-21  
12 PRIOR APPLICATION NUMBER: 60/077450  
13 PRIOR FILING DATE: 1998-03-10  
14 PRIOR APPLICATION NUMBER: 60/077632  
15 PRIOR FILING DATE: 1998-03-11  
16 PRIOR APPLICATION NUMBER: 60/077641  
17 PRIOR FILING DATE: 1998-03-11  
18 PRIOR APPLICATION NUMBER: 60/077649  
19 PRIOR FILING DATE: 1998-03-11  
20 PRIOR APPLICATION NUMBER: 60/077791  
21 PRIOR FILING DATE: 1998-03-12  
22 PRIOR APPLICATION NUMBER: 60/078004  
23 PRIOR FILING DATE: 1998-03-13  
24 PRIOR APPLICATION NUMBER: 60/078886  
25 PRIOR FILING DATE: 1998-03-20  
26 PRIOR APPLICATION NUMBER: 60/078936  
27 PRIOR FILING DATE: 1998-03-20  
28 PRIOR APPLICATION NUMBER: 60/078910  
29 PRIOR FILING DATE: 1998-03-20  
30 PRIOR APPLICATION NUMBER: 60/078939  
31 PRIOR FILING DATE: 1998-03-20  
32 PRIOR APPLICATION NUMBER: 60/079294  
33 PRIOR FILING DATE: 1998-03-25  
34 PRIOR APPLICATION NUMBER: 60/079656  
35 PRIOR FILING DATE: 1998-03-26  
36 PRIOR APPLICATION NUMBER: 60/079664  
37 PRIOR FILING DATE: 1998-03-27  
38 PRIOR APPLICATION NUMBER: 60/079689  
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41 PRIOR FILING DATE: 1998-03-27  
42 PRIOR APPLICATION NUMBER: 60/079728  
43 PRIOR FILING DATE: 1998-03-27  
44 PRIOR APPLICATION NUMBER: 60/079786  
45 PRIOR FILING DATE: 1998-03-27  
46 PRIOR APPLICATION NUMBER: 60/079920  
47 PRIOR FILING DATE: 1998-03-30  
48 PRIOR APPLICATION NUMBER: 60/079923  
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51 PRIOR FILING DATE: 1998-03-31  
52 PRIOR APPLICATION NUMBER: 60/080107  
53 PRIOR FILING DATE: 1998-03-31  
54 PRIOR APPLICATION NUMBER: 60/080165  
55 PRIOR FILING DATE: 1998-03-31  
56 PRIOR APPLICATION NUMBER: 60/080194  
57 PRIOR FILING DATE: 1998-03-31  
58 PRIOR APPLICATION NUMBER: 60/080327  
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80 PRIOR APPLICATION NUMBER: 60/081817  
81 PRIOR FILING DATE: 1998-04-15  
82 PRIOR APPLICATION NUMBER: 60/081819  
83 PRIOR FILING DATE: 1998-04-15  
84 PRIOR APPLICATION NUMBER: 60/081952  
85 PRIOR FILING DATE: 1998-04-15  
86 PRIOR APPLICATION NUMBER: 60/081838  
87 PRIOR FILING DATE: 1998-04-15  
88 PRIOR APPLICATION NUMBER: 60/082568  
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93 PRIOR FILING DATE: 1998-04-22  
94 PRIOR APPLICATION NUMBER: 60/082804  
95 PRIOR FILING DATE: 1998-04-22  
96 PRIOR APPLICATION NUMBER: 60/082700  
97 PRIOR FILING DATE: 1998-04-22  
98 PRIOR APPLICATION NUMBER: 60/082797  
99 PRIOR FILING DATE: 1998-04-22  
100 PRIOR APPLICATION NUMBER: 60/082796  
101 PRIOR FILING DATE: 1998-04-23  
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103 PRIOR FILING DATE: 1998-04-27  
104 PRIOR APPLICATION NUMBER: 60/083322  
105 PRIOR FILING DATE: 1998-04-28  
106 PRIOR APPLICATION NUMBER: 60/083392  
107 PRIOR FILING DATE: 1998-04-29  
108 PRIOR APPLICATION NUMBER: 60/083495  
109 PRIOR FILING DATE: 1998-04-29  
110 PRIOR APPLICATION NUMBER: 60/083496  
111 PRIOR FILING DATE: 1998-04-29  
112 PRIOR APPLICATION NUMBER: 60/083499  
113 PRIOR FILING DATE: 1998-04-29  
114 PRIOR APPLICATION NUMBER: 60/083545  
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116 PRIOR APPLICATION NUMBER: 60/083554  
117 PRIOR FILING DATE: 1998-04-29  
118 PRIOR APPLICATION NUMBER: 60/083558  
119 PRIOR FILING DATE: 1998-04-29  
120 PRIOR APPLICATION NUMBER: 60/083559  
121 PRIOR FILING DATE: 1998-04-29  
122 PRIOR APPLICATION NUMBER: 60/083500  
123 PRIOR FILING DATE: 1998-04-29  
124 PRIOR APPLICATION NUMBER: 60/083742  
125 PRIOR FILING DATE: 1998-04-30  
126 PRIOR APPLICATION NUMBER: 60/084366  
127 PRIOR FILING DATE: 1998-05-05  
128 PRIOR APPLICATION NUMBER: 60/084414  
129 PRIOR FILING DATE: 1998-05-06  
130 PRIOR APPLICATION NUMBER: 60/084441  
131 PRIOR FILING DATE: 1998-05-06  
132 PRIOR APPLICATION NUMBER: 60/084637  
133 PRIOR FILING DATE: 1998-05-07  
134 PRIOR APPLICATION NUMBER: 60/084639  
135 PRIOR FILING DATE: 1998-05-07  
136 PRIOR APPLICATION NUMBER: 60/084640  
137 PRIOR FILING DATE: 1998-05-07  
138 PRIOR APPLICATION NUMBER: 60/084598  
139 PRIOR FILING DATE: 1998-05-07  
140 PRIOR APPLICATION NUMBER: 60/084600  
141 PRIOR FILING DATE: 1998-5-07  
142 PRIOR APPLICATION NUMBER: 60/084627  
143 PRIOR FILING DATE: 1998-05-07  
144 PRIOR APPLICATION NUMBER: 60/084643  
145 PRIOR FILING DATE: 1998-05-07  
146 PRIOR APPLICATION NUMBER: 60/085339

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; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085338
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
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; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-189-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCACTCCAGCAAAATGCAATCTCTCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GTGCTCTGTGCTCTCTCAAGAGAGTGGCCGTGGCAGCGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGACAAGTACGGTCCGGCAGGGAGGAGCGCCACCTCAGGTGCATATGTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AGTGTGCTGTGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTGGATGTGTATGACAGGGGCCCTTACCTGCTCGGTGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCCCAAGACCTTAGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCCTACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGGGGTTCGCTTTGTG 673
QY 181 SerGluAspGlnTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACCAATATCTTGAATATTCAGGCATCACCGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValThrValAsn 220
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Db 734 TGCAGTGCCTCCATGACGTGGCCGCCGTGGTACGAGAGTAAGGTCAACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAGAACCCAGGTAACAGGTGTCCCGCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260
Db 854 CTGCGAGTGTGAAGCCTTCAGAGTCCCTCAGCAGCAATTCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGAAACAGACCTTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGGTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGGTCCAGGCCCGCTCAGCGAGGTGACC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
Db 1094 AACGGCACGTGCAGGAGGAGGAGGCTGGCTGTGGCTGTGGCTCTTCTTGTGTTGCACCTG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 7
US-09-978-608A-522
; Sequence 522, Application US/09978608A
; Publication No. US20030045462A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PLC22
; CURRENT APPLICATION NUMBER: US/09/978,608A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
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US-09-978-608A-522

## Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-608A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
Db 134 ATGAACCATCCAGCAAAATGCAATCTATCTCTTGGCAATCTTCAAGGGGTG 193  
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
Db 194 GCTGCTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253  
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
Db 254 GCTATGGCAACGTCACGCTCCGCGGGGAGAGCCACCTCAGGTGCACATTATGAC 313  
Qy 61 AsnArgValThrArgValAlaIlePheLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
Db 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373  
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrSerIle 100  
Db 374 AAGTGGTCCCTGGATCCCTCGCGTGTCTCTCTAGCAACACCCAAACGACGTACGATC 433  
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 434 GAGATCCAGACGTCGATGTATGACGAGGCGCTTACCTGCTCCGTGCGACACAC 493  
Qy 121 AsnHisProLysThrSerArgValHisLeulleValGlnValSerProLysIleValGlu 140  
Db 494 AACCAACCAAGACCTCTAGGTCACCTCTATGTCAGATATCTCCCAAAATGTAGAG 553  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160  
Db 554 ATTTCTTCAGATATCTCATTAATGAAGGGAACAATATTAGCTCACCCTGCATAGCACT 613  
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db 614 GGTAGACCAAGACCTTACGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673  
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGGACTACGAG 733  
Qy 201 CysSerAlaSerAsnAspValAlaIleProValValArgArgValLysValThrValAsn 220  
Db 734 TGCAGTGCCTCAATGAGTCGCGCGCGGTGACGAGAGTAAGGTACCGGTGAAC 793  
Qy 221 TyrProTrpTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 794 TATCCACCATATCTTCAAGAGCCAGGTACAGGTGTCCCGTGGGCAAAAGGGGACA 853  
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260  
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATCCAGTGTGTACAGGATGACAA 913  
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 AGACTGATTTGAAGGAAAGAAAGGGGTGAAGTGAAGTGAAGAAACAGACCTTCTCTCAAACTC 973  
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTCTTCAATGTCTCTGAACATGACTATGGGAACACTACATCTGGCTGGCTCCCAAG 1033  
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320

Db 1034 CTGGGCACACCAATGCCAGATCATGCTATTGGTCAGGCGCGTCAGCGAGGTGAC 1093  
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340  
Db 1094 AACGGCAGCTCAGAGAGGAGGCTGGCTCTGGCTGTGCTCTTCTGTCTTGCACCTG 1153  
Qy 341 LeuLeuLysPhe 344  
Db 1154 CTTCTCAAAATTT 1165

## RESULT 8

US-09-978-585A-522  
; Sequence 522, Application US/09978585A  
; Publication No. US20030049633A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnovers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C15  
; CURRENT APPLICATION NUMBER: US/09/978,585A  
; PRIORITY FILING DATE: 2001-10-16  
; NUMBER OF SEQ ID NOS: 624  
; Prior Application removed - See File Wrapper or Palm  
; SEQ ID NO 522  
; LENGTH: 1679  
; TYPE: DNA  
; ORGANISM: Homo sapiens

US-09-978-585A-522

## Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservatives: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-585A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
Db 134 ATGAACCATCCAGCAAAATGCAATCTATCTTGGCAATCTTCAAGGGGTG 193  
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
Db 194 GCTGCTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGGAGATGCCACCTTCCCAA 253

QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
Db 254 GCTATGGACACGTGACGGTCCGGCAGGGGAGAGCCACCTCAGTGCATATTGAC 313  
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
Db 314 AACCGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373  
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
Db 374 AAGTGGTGGCTGGATCTCCGGTGGCTCTCTGAGCAACACCCAAACGGCAGTACGATC 433  
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGTGGCAGACGAC 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTGTAGAG 553  
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 554 ATTCTTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCCTGCATAGCAACT 613  
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db 614 GGTAGACCAAGCTACGGTTACTTGTGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673  
QY 181 SerGluAspGlnTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 674 AGTGAAGACCAAACTTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACGAG 733  
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220  
Db 734 TGAGTGCCTCCATGACGTGGCGCGCCGCGTGTGAGAGAGTAAAGGTACCGTGAAC 793  
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 794 TATCCACCATACATTTTCAGAAAGCCAGGGTACAGGTGTCCCCGTGGGACAAAGGGGACA 853  
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260  
Db 854 CTGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGGTGGTCAAGAGATGACAAA 913  
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 AGACTGATTGAAGAAAGAGGGGTGAAGTGAAGAACAGACCTTCTCTCAAACTC 973  
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTCTCTCAATGTCTCTGAACATGACTATGGGAACCTACACTTGGCGTGGCTCCAAAG 1033  
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
Db 1034 CTGGGCCACCAATGCGCATCATCTATTGGTCCAGCGCCGTCAGCGAGGTGAGC 1093  
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340  
Db 1094 AACGGCAGTCGAGGAGGGCAGGTGCTGCTGGCTGCTCTCTCTGGTCTTGGTCTTGCACCTG 1153  
QY 341 LeuLeuLysPhe 344  
Db 1154 CTCTCAAAATTT 1165

## RESULT 9

US-09-978-191A-522

; Sequence 522, Application US/09978191A

; Publication No. US20030050239A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C4  
; CURRENT APPLICATION NUMBER: US/09/978,191A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
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/ PRIOR APPLICATION NUMBER: 60/082700  
/ PRIOR FILING DATE: 1998-04-22  
/ PRIOR APPLICATION NUMBER: 60/082797  
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/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085704  
/ PRIOR FILING DATE: 1998-05-15  
/ PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-191A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCAAAATGCAAAATTCATCTCTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTGTGTCTCTTCCAAAGGAGTGCCCGGCGAGGATGCCACCTTCCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGTCGCGCAGGGGAGAGCCACCTCAGTGCACATTGCAC	313
QY	61	AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80

Db 314 AACGGGTGTCACCCGGGTGGCCCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373  
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
Db 374 AAGTGGTGGCTGGATCCTCGCGTGGTCTCTCTGAGCAACACCCAAAGCGAGTACAGCATC 433  
Qy 101 GlutIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
Db 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACCTGCTGCTGGTCCACAGAC 493  
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db 494 AACCAACCAAGACCTCTAGGCTCCACCTATTGTGCAAGTATCTCCCAAAATTTGTAGAG 553  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 554 ATTTCTTCAGATATCTCCATTAAATGAAGGGAAACAATATTAGCCCTCACCTGATAGCACT 613  
Qy 161 GlyArgProGluProThrValThrTyrArgHisIleSerProLysAlaValGlyPheVal 180  
Db 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673  
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733  
Qy 201 CysSerAlaSerAsnAspValAlaAalaProValValArgArgValLysValThrValAsn 220  
Db 734 TGCAGTGCCTCCATGACGTGGCCGCGCCGTGGTACGGAGATGAAGTCAACGTGAAC 793  
Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 794 TATCCACCATACATTTCCAGAACCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853  
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspAspLys 260  
Db 854 CTGAGTGTGAAGCCTTCAGCAGTCCCTTCAGCAGAAATTCAGTGGCTCCCAACAAAG 913  
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 AGACTGATTGAAGGAAGAGGGGTGAAGTGGAAACACAGACCTTCTCTCAAACTC 973  
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTTCTCAATGCTCTCGAACATGACTATGGAACTACTTGGTGGCTCCCAACAAAG 1033  
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
Db 1034 CTGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCCGTGAGGAGTGAGC 1093  
Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340  
Db 1094 AACGSCAGTCGAGGAGGCGAGGCTGGCTGGCTGCTGCTCTTCTGCTTGTGACCTG 1153  
Qy 341 LeuLeuLysPhe 344  
Db 1154 CTTCCTCAAAATTT 1165

RESULT 10  
US-09-978-403A-522  
; Sequence 522, Application US/09978403A  
; Publication No. US20030050240A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C17  
; CURRENT APPLICATION NUMBER: US/09/978,403A  
; CURRENT FILING DATE: 2002-03-19  
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32 PRIOR FILING DATE: 1998-05-15  
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36 PRIOR FILING DATE: 1998-05-15  
37 PRIOR APPLICATION NUMBER: 60/085573  
38 PRIOR FILING DATE: 1998-05-15  
39 PRIOR APPLICATION NUMBER: 60/085704  
40 PRIOR FILING DATE: 1998-05-15  
41 PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	1,19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-403A-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMethHisAsnSerIleSerThrAlaIlePheThrGlyLeu	20
DB	134	ATGAAACCATCCAGCAAAATGCACAAATCTATCTCTGGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAGAGATGCCCGCGCGGAGATGCCACCTTCCCAAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGGTCCGCGAGGAGAGCGCACCTCAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaIleThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp	80
DB	314	AAACCGGTTCACCGGGTGGCTGGTAAACCGCACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGGTGGCTGGATCTCGGTGGTCTCTTCAGACCAACCCAAACGAGATCAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120

Db 434 GAGATCCAGAACGCTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCGACAGAC 493  
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
Db 494 AACCAACCAAGACCTCTAGGGTCCACCTATTGTGCAAGTATCTCCAAAATTGTAGAG 553  
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGGAACAATATTAGCCTCACCTGCATAGCAACT 613  
Qy 161 GlyArgProGluProThrValThrTriArgHisIleSerProLysAlaValGlyPheVal 180  
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Qy 181 SerGluAspGluThrLeuGluIleGlnIleThrArgGluGlnSerGlyAspTyrGlu 200  
Db 674 AGTAGAGACGAATACTTGGAAATTCAGGGCATCCCGGGAGCAGTCAGGGGACTACGAG 733  
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Qy 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 794 TATCCACCATACATTCAGAGCCACAGGTTACAGGTGTCCCGTGGACAAAAGGGGACA 853  
Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrLysAspAspLys 260  
Db 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTCAAGGATGACAAA 913  
Qy 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 ACATGATTGAAGGAAGAAGGGGTGAAGTGGAAACACAGCTTCTCTCAAAACTC 973  
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTTCTCAATGCTCTGAAACATGACTATGGGAATACACTTGGTGGCTCCCAACAAG 1033  
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
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Qy 321 AsnGlyThrSerArgArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340  
Db 1094 AACGGCAGTCCGAGGAGGGGCGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153  
Qy 341 LeuLeuLysPhe 344  
Db 1154 CTCTCAAAATTT 1165

## RESULT 11

US-09-978-564A-522

; Sequence 522, Application US/09978564A

; Publication No. US20030050241A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan

; APPLICANT: Ferrara, Napoleon

; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Kljavin, Ivar J.

; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630PIC25  
; CURRENT APPLICATION NUMBER: US/09/978,564A  
; CURRENT FILING DATE: 2001-10-16  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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5 PRIOR APPLICATION NUMBER: 60/080334  
6 PRIOR FILING DATE: 1998-04-01  
7 PRIOR APPLICATION NUMBER: 60/081070  
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14 PRIOR FILING DATE: 1998-04-08  
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16 PRIOR FILING DATE: 1998-04-09  
17 PRIOR APPLICATION NUMBER: 60/081229  
18 PRIOR FILING DATE: 1998-04-09  
19 PRIOR APPLICATION NUMBER: 60/081955  
20 PRIOR FILING DATE: 1998-04-15  
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22 PRIOR FILING DATE: 1998-04-15  
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26 PRIOR FILING DATE: 1998-04-15  
27 PRIOR APPLICATION NUMBER: 60/081838  
28 PRIOR FILING DATE: 1998-04-15  
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32 PRIOR FILING DATE: 1998-04-21  
33 PRIOR APPLICATION NUMBER: 60/082704  
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35 PRIOR APPLICATION NUMBER: 60/082804  
36 PRIOR FILING DATE: 1998-04-22  
37 PRIOR APPLICATION NUMBER: 60/082700  
38 PRIOR FILING DATE: 1998-04-22  
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41 PRIOR APPLICATION NUMBER: 60/082796  
42 PRIOR FILING DATE: 1998-04-23  
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44 PRIOR FILING DATE: 1998-04-27  
45 PRIOR APPLICATION NUMBER: 60/083322  
46 PRIOR FILING DATE: 1998-04-28  
47 PRIOR APPLICATION NUMBER: 60/083332  
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61 PRIOR APPLICATION NUMBER: 60/083559  
62 PRIOR FILING DATE: 1998-04-29  
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64 PRIOR FILING DATE: 1998-04-29  
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66 PRIOR FILING DATE: 1998-04-30  
67 PRIOR APPLICATION NUMBER: 60/084366  
68 PRIOR FILING DATE: 1998-05-05  
69 PRIOR APPLICATION NUMBER: 60/084414  
70 PRIOR FILING DATE: 1998-05-06  
71 PRIOR APPLICATION NUMBER: 60/084441  
72 PRIOR FILING DATE: 1998-05-06  
73 PRIOR APPLICATION NUMBER: 60/084637

1 PRIOR FILING DATE: 1998-05-07  
2 PRIOR APPLICATION NUMBER: 60/084639  
3 PRIOR FILING DATE: 1998-05-07  
4 PRIOR APPLICATION NUMBER: 60/084640  
5 PRIOR FILING DATE: 1998-05-07  
6 PRIOR APPLICATION NUMBER: 60/084598  
7 PRIOR FILING DATE: 1998-05-07  
8 PRIOR APPLICATION NUMBER: 60/084600  
9 PRIOR FILING DATE: 1998-05-07  
10 PRIOR APPLICATION NUMBER: 60/084627  
11 PRIOR FILING DATE: 1998-05-07  
12 PRIOR APPLICATION NUMBER: 60/084643  
13 PRIOR FILING DATE: 1998-05-07  
14 PRIOR APPLICATION NUMBER: 60/085339  
15 PRIOR FILING DATE: 1998-05-13  
16 PRIOR APPLICATION NUMBER: 60/085338  
17 PRIOR FILING DATE: 1998-05-13  
18 PRIOR APPLICATION NUMBER: 60/085323  
19 PRIOR FILING DATE: 1998-05-13  
20 PRIOR APPLICATION NUMBER: 60/085582  
21 PRIOR FILING DATE: 1998-05-15  
22 PRIOR APPLICATION NUMBER: 60/085700  
23 PRIOR FILING DATE: 1998-05-15  
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26 PRIOR APPLICATION NUMBER: 60/085579  
27 PRIOR FILING DATE: 1998-05-15  
28 PRIOR APPLICATION NUMBER: 60/085580  
29 PRIOR FILING DATE: 1998-05-15  
30 PRIOR APPLICATION NUMBER: 60/085573  
31 PRIOR FILING DATE: 1998-05-15  
32 PRIOR APPLICATION NUMBER: 60/085704  
33 PRIOR FILING DATE: 1998-05-15  
34 PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 1.19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-564A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethIleAsnSerIleSerThrAlaIlePheThrGlyLeu 20  
DB 134 ATGAAACCATCCAGCAAAATGCACAAATTCATCTCTTGGGCAATCTTCACGGGGCTG 193  
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
DB 194 GCTGCTCTGTGTCTCTTCCAGGAGTGCCCGTGGCAGCGGAGATGCCACCTTCCCAAA 253  
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
DB 254 GCTATGGACACAGTCAGCGTCGGCAGCGGAGAGCGCCACCTCAGGTGCTATTGAC 313  
QY 61 AsnArgValThrArgValAlaIleLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
DB 314 AACCGGGTCACCGGGGTGGCCCTGAAACCCAGCAGCACCCTCTATCTCTGGGAATGAC 373  
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
DB 374 AAGTGGTGTGATCCTCGCTGCTCTTCTTGAGCAACACCCCAACGAGTACAGCATC 433  
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
DB 434 GAGATCCAGACGTGGATGTGTATCAGGAGGGCCCTTACACCTGCTCGTGGTGCAGACAG 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
DB 494 AACCAACCAAGACCTTAGGGTCCACCTCATTTGTGAAGTAGTATCTCCCAAAATTTAGAG 553

Qy	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTTCTTCAGATAATCTCATTAATGAAGGGAAACAATATTAGCCTCACTGCATAGCAACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GGTAGACACAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG	673
Qy	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
Db	674	AGTGAAGACGAATACTTTGGAAATTCAGGGCATCACCCGGGAGCAGTACGGGACATACGAG	733
Qy	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
Db	734	TGCAGTGCCTCCAATGACGTGGCGCGCGCGTGTGTACGGAGAGTAAAGETCACCGTGAAC	793
Qy	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
Db	794	TATCCACCATACATTTTCAAGAGCCACGGGTACAGTGTCCCGGTGGGCAAAAGGGGACA	853
Qy	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys	260
Db	854	CTGCAGTGTGAAGCGCTCAGCAGTCCCTCTCAGCAGAAATTCACAGTGGTACACAGGATGACAAA	913
Qy	261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysIleu	280
Db	914	AGACTGATTGAAAGAAAGAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAATCTC	973
Qy	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
Db	974	ATCTTCTTCAATGTCTCTGAACATGACTATGGGAACACTACATTGCGTGGCCTCCACACAG	1033
Qy	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
Db	1034	CTGGGCGACACCAATGCCAGCATCATGCTATTGTGTCAGGCGCGCTCAGCGAGGTGAGC	1093
Qy	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisIleu	340
Db	1094	AACGGCACGTGAGAGGGCAGGCTGCCTCTGCTGTGCGCTCTTCTGGTCTTCACACTG	1153
Qy	341	LeuLeuLysPhe	344
Db	1154	CTTCTCTCAAAATTT	1165

RESULT 12

US-09-999-833A-522  
; Sequence 522, Application US/09999833A  
; Publication No. US20030054405A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas P.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.



1	PRIOR FILING DATE: 1998-04-08	
2	PRIOR APPLICATION NUMBER: 60/081049	
3	PRIOR FILING DATE: 1998-04-08	
4	PRIOR APPLICATION NUMBER: 60/081071	
5	PRIOR FILING DATE: 1998-04-08	
6	PRIOR APPLICATION NUMBER: 60/081195	
7	PRIOR FILING DATE: 1998-04-08	
8	PRIOR APPLICATION NUMBER: 60/081203	
9	PRIOR FILING DATE: 1998-04-09	
10	PRIOR APPLICATION NUMBER: 60/081229	
11	PRIOR FILING DATE: 1998-04-09	
12	PRIOR APPLICATION NUMBER: 60/081955	
13	PRIOR FILING DATE: 1998-04-15	
14	PRIOR APPLICATION NUMBER: 60/081817	
15	PRIOR FILING DATE: 1998-04-15	
16	PRIOR APPLICATION NUMBER: 60/081819	
17	PRIOR FILING DATE: 1998-04-15	
18	PRIOR APPLICATION NUMBER: 60/081952	
19	PRIOR FILING DATE: 1998-04-15	
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22	PRIOR APPLICATION NUMBER: 60/082568	
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72	PRIOR APPLICATION NUMBER: 60/084598	
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?	PRIOR FILING DATE:	1998-05-13
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?	PRIOR FILING DATE:	1998-05-15
?	PRIOR APPLICATION NUMBER:	60/085704
?	PRIOR FILING DATE:	1998-05-15
?	PRIOR APPLICATION NUMBER:	60/085697

Alignment Scores:

Alignment Scores:		
Pred. No.:	1,19e-41	1679
Score:	2408.00	344
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	100.00%	Indels: 0
DB:	10	Gaps: 0

US-10-017-084A-523 (1-344) X US-09-999-833A-522 (1-1679)

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Db	134	ATGAACACCATCAGCCAAAATGACAAATTCATCTCTTGGCAATCTCTCAGGGGCTG	193
Qy	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTGTGTCTCTTCCAGAGATGCCGTGGCGACGGAGATGCCACCTTCCCNAA	253
Qy	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGGACAACGTGACCGTCCGGCAGGGGAGAGCGCCACCTCTCAGTGTCATTTGAC	313
Qy	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
Db	314	AACCGGTCCACCGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC	373
Qy	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTySerIle	100
Db	374	AACTGTGTGCTGGATCCTCGGTGTGTCTCTGAGCAACACCCAAACGCAGTACAGCATC	433
Qy	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
Db	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
Qy	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db	494	AAACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG	553
Qy	141	IleSerSerAspIleSerIleAsnGluClyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db	554	ATTCTTTCAGATATCTCCATTAATGAGGGGAACAATATTAGCCTCACCTCATTAGCAACT	613
Qy	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db	614	GGTAGACAGAGCTACGGTACTTTGACAGACATCTCTCCCAAGCGGGGCTTTTGG	673

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QY 181 SerGluAspGluTyrLeuGluIleGlnGlyThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCGGAGCAGTCAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgGluValValThrValAsn 220
Db 734 TGCAGTGCTTCAATGAGTGCGGCCCGCGGAGTACGAGGAGTAAAGGTACCGGTGAAC 793
QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCACCATACATTTTCAGAACCCAGGATACAGGTGTCCCGTGGACAAAAGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrIleAspLys 260
Db 854 CTGCGAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGATCAAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTTGAAGGAAAGAAAGGGTGAAGTGGAAACAGACACCTTCTCTCAAAATC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 ATCTCTTCAATGTCTCTGAACATGACTATGGGAACTACACTTGGTGGCCTCCCAACAAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTATTTGGTCCAGGCGCGTCAGCGAGTGAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCAGCTCAGAGGGGAGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTCTCAAAATTT 1165

RESULT 13
US-09-981-915A-522
; Sequence 522, Application US/09981915A
; Publication NO. US20030054986A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PlC12
; CURRENT APPLICATION NUMBER: US/09/981,915A
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/ PRIOR APPLICATION NUMBER: 60/081229
/ PRIOR FILING DATE: 1998-04-09
/ PRIOR APPLICATION NUMBER: 60/081955
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/ PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:      1.19e-41      Length:      1679
Score:          2408.00      Matches:    344
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:               10          Gaps:        0

US-10-017-084A-523 (1-344) x US-09-981-915A-522 (1-1679)
QY      1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB      134 ATGAARACCATCCAGCCAAATATGCAATTTCTATCTTGGCAATCTTCACGGGGCTG 193
QY      21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB      194 GCTGCTCTGTCTCTTCCAGGAGTGCCGTCGCGAGGAGATGCCACCTTCCCAAA 253
QY      41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB      254 GCTATGCAACAGTGACGTCCGCTCCGGCAGGGGAGAGGCCACCTCAGGTGCATATTGAC 313
QY      61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
DB      314 AACCGGGTCACCGGGTGCGCTGGCTAAACCGCAGACCATCTCTATGCTGGGATGAC 373
QY      81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100
DB      374 AAGTGGTGCTGGATCCTCGCGTGGTCTTCTGAGCAACACCCAAACGAGTACAGCATC 433
QY      101 GluIleGlnAsnValAspValTrpAspGluGlyProTrpThrCysSerValGlnThrAsp 120
DB      434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAG 493
QY      121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB      494 AACCCCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATTTAGAG 553
QY      141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB      554 ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGCAACT 613
QY      161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB      614 GGTAGACCAAGAGCCTACGGTTACTTGGAGACACATCTCTCCAAACGGTGTGGCTTTGG 673
QY      181 SerGluAspGluTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200
DB      674 AGTGAAGACGAATACTTGGAAATTCAGGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733
QY      201 CysSerAlaSerAsnAspValAlaIleProValValArgArgValLysValThrValAsn 220
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Db 794 TATCACCACATACATTTCAGAACCCCAAGGGTACAGGTGTCCCGTGGGACAAAAGGGGACA 853  
QY LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrTyrAspAspLys 260  
Db 854 CTGCGAGTGTGAAGCTTCAGCACTCCCTCAGCAGAAATTCAGTGTGATCAAGATGACAAA 913  
QY ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 AGACTGATTAAGAGGAAGAGCGGTGAAAGTGGAAACAGACCTTTCTCTCAAAACTC 973  
QY IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTCTCTTCAATGTCTCTGAACATGACTATGGGAACACTACCTTCGCTGGCTCCCAACAG 1033  
QY LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320  
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTTGGTCCAGGCGCGTACGGAGTGAAC 1093  
QY AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuValLeuHisLeu 340  
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QY LeuLeuLysPhe 344  
Db 1154 CTCTCAAAATTT 1165  
RESULT 14  
US-09-978-824-522  
; Sequence 522, Application US/09978824  
; Publication No. US20030055216A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: William, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC14  
; CURRENT APPLICATION NUMBER: US/09/978,824  
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; PRIOR FILING DATE: 2001-07-30  
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; PRIOR APPLICATION NUMBER: 60/085704  
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; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-824-522 (1-1679)

QY	1	MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu	20
DB	134	ATGAATACCATCCAGCCAAAATGCAATTCATCTCTTGGCAATCTTCACGGGGCTG	193
QY	21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
DB	194	GCTGCTCTGTCTCTTCCAAAGGAGTGCCGTGCGGAGGAGATGCCACCTTCCCNAA	253
QY	41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
DB	254	GCTATGGACAACGTGACGGTCCGGGAGGAGCGCCACCTCCTAGGTGCATATTGAC	313
QY	61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuValAlaGlyAsnAsp	80
DB	314	AACCGGGTCACCGGGTGGCTGGCTAAACCGGAGACCATCTCTATGCTGGGAATGAC	373
QY	81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
DB	374	AAGTGGTGCTGGATCTCGCGTGGTCTTCTGAGCAACACCCAAACGGCAGTACAGCATC	433
QY	101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
DB	434	GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCCCTTACACCTGCTCGGTGACAGAC	493
QY	121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
DB	494	AACCAACCAAGACCTTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTTAGAG	553
QY	141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
DB	554	ATTCTCTCAGATATCTCCATTAATGAAGGGAACAATATTAGCCTCACCTGCATAGAACT	613
QY	161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
DB	614	GGTAGACCAAGCCTACGGTTACTTGGAGACACATCTCTCCAAACGGGTGGCTTTGTG	673
QY	181	SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu	200
DB	674	AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACGAG	733
QY	201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn	220
DB	734	TGCAGTGCCTCCAATGACGTGGCCGCGCGGTGGTACCGGAGAGTAAGGTCAACCGTAAC	793
QY	221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
DB	794	TATCCACCATATATTTCAAGCAAGGAGGTACAGGTGTCCTCCCGTGGGACAAAGGGGACA	853
QY	241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys	260

Db 854 CTCGAGTGTGAAGCCTCAGCAGTCCCTCCAGCAGAAATTCAGTGTGTAACAGATGACAAA 913  
Qy 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
Db 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACACAGACCTTTCTCTCAAAATCTC 973  
Qy 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
Db 974 ATCTTCTTCAATGCTCTCTGAACATGACTATGGGAACACTACCTGCGTGGCCCTCCCAACAAG 1033  
Qy 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
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Db 1094 AACGGCAGCTCGAGGAGGAGGCTGCGTCTGGCTGCTTCTGGTCTTCTGGTCTTGCACCTG 1153  
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Db 1154 CTTCTCAAAATTT 1165

RESULT 15  
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; Publication No. US20030060406A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C1  
; CURRENT APPLICATION NUMBER: US/09/918,585A  
; CURRENT FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
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10 PRIOR FILING DATE: 1998-04-22  
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17 PRIOR APPLICATION NUMBER: 60/083392  
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43 PRIOR APPLICATION NUMBER: 60/084637  
44 PRIOR FILING DATE: 1998-05-07  
45 PRIOR APPLICATION NUMBER: 60/084639  
46 PRIOR FILING DATE: 1998-05-07  
47 PRIOR APPLICATION NUMBER: 60/084640  
48 PRIOR FILING DATE: 1998-05-07  
49 PRIOR APPLICATION NUMBER: 60/084598  
50 PRIOR FILING DATE: 1998-05-07  
51 PRIOR APPLICATION NUMBER: 60/084600  
52 PRIOR FILING DATE: 1998-05-07  
53 PRIOR APPLICATION NUMBER: 60/084627  
54 PRIOR FILING DATE: 1998-05-07  
55 PRIOR APPLICATION NUMBER: 60/084643  
56 PRIOR FILING DATE: 1998-05-07  
57 PRIOR APPLICATION NUMBER: 60/085339  
58 PRIOR FILING DATE: 1998-05-13  
59 PRIOR APPLICATION NUMBER: 60/085338  
60 PRIOR FILING DATE: 1998-05-13  
61 PRIOR APPLICATION NUMBER: 60/085323  
62 PRIOR FILING DATE: 1998-05-13  
63 PRIOR APPLICATION NUMBER: 60/085582  
64 PRIOR FILING DATE: 1998-05-15  
65 PRIOR APPLICATION NUMBER: 60/085700  
66 PRIOR FILING DATE: 1998-05-15  
67 PRIOR APPLICATION NUMBER: 60/085689  
68 PRIOR FILING DATE: 1998-05-15  
69 PRIOR APPLICATION NUMBER: 60/085579  
70 PRIOR FILING DATE: 1998-05-15  
71 PRIOR APPLICATION NUMBER: 60/085580  
72 PRIOR FILING DATE: 1998-05-15  
73 PRIOR APPLICATION NUMBER: 60/085573

1 PRIOR FILING DATE: 1998-05-15  
2 PRIOR APPLICATION NUMBER: 60/085704  
3 PRIOR FILING DATE: 1998-05-15  
4 PRIOR APPLICATION NUMBER: 60/085697  
5 PRIOR FILING DATE: 1998-05-15  
6 PRIOR APPLICATION NUMBER: 60/086023

## Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservative: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-918-585A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMethHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
DB 134 ATGAAACCATCCAGCCAAAATGCACAATCTATCTCTTGGCAATCTTCACGGGGCTG 193  
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
DB 194 GGTGCTCTGTCTCTTCCAGGAGTGCCTGCGCAGCGAGATGCCACCTTCCCAAA 253  
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
DB 254 GCTATGGACAACGTGACGGTCCGGCAGGGGGAGAGGCCACCCCTCAGGTGCACATTGAC 313  
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
DB 314 AACCGGTCACCGGGTGGCTGGCTAAACCCGAGCAGCACCATCTCTATGCTGGGAATGAC 373  
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
DB 374 AAGTGGTGCCTGGATCCTCGCGTGGTTCCTGAGCAACACCCAAACGAGTACAGCATC 433  
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCAITGTGCAAGTATCTCCCAAAATGTAGAG 553  
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerIleThrCysIleAlaThr 160  
DB 554 ATTTCTTCAGATATCTCCATTAATGAAGGAACAATATTAGCCTCACCTGCATAGCACT 613  
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
DB 614 GGTAGACCAAGCGCTACGGTTACTTTGGAGACACATCTCTCCCAACGCGTGGCTTTGTG 673  
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCACGGGACTACGAG 733  
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220  
DB 734 TGCAGTGCCTCCATGACGTGGCCGCCCGCTGGTACGGAGAGTAAAGGTACCGTGAAC 793  
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
DB 794 TATCCACCACATATTCAGAAGCAAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853  
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260  
DB 854 CTGCAGTGTGAAGCCCTCAGCAGTCCCTCAGCAGATTCOAGTGGTACAGGATGACAAA 913  
QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
DB 914 AGACTGATTGAAGGAAGAAGGGTGAAGTGGAAACACAGACCTTCTCTCAAAACATC 973

QY	281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnIys	300	PRIOR APPLICATION NUMBER: 60/078004
				PRIOR FILING DATE: 1998-03-13
Db	974	ATCTCTTCAATGTCTCTGAACATGACATATGGAACTACATTCGGTGGCCCTCAACAAG	1033	PRIOR APPLICATION NUMBER: 60/078886
				PRIOR FILING DATE: 1998-03-20
QY	301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320	PRIOR APPLICATION NUMBER: 60/078936
				PRIOR FILING DATE: 1998-03-20
Db	1034	CTGGGCCACACCAATGCCAGCATCATGCTATTGTGTCAGGGCGGTCAGCGAGGTGAGC	1093	PRIOR APPLICATION NUMBER: 60/078910
				PRIOR FILING DATE: 1998-03-20
QY	321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisIeu	340	PRIOR APPLICATION NUMBER: 60/078939
				PRIOR FILING DATE: 1998-03-20
Db	1094	AACGGCACGTCGAGGAGGCGAGCTGCTGCTGCTCTTCTGCTTGCACCTG	1153	PRIOR APPLICATION NUMBER: 60/079294
				PRIOR FILING DATE: 1998-03-25
QY	341	LeuLeuIlyaphe	344	PRIOR APPLICATION NUMBER: 60/079656
				PRIOR FILING DATE: 1998-03-26
Db	1154	CTTCTCAATTT	1165	PRIOR APPLICATION NUMBER: 60/079664
				PRIOR FILING DATE: 1998-03-27
RESULT 16				
US-09-978-423A-522				
Sequence 522, Application US/09978423A				
Publication No. US20030069178A1				
GENERAL INFORMATION:				
		APPLICANT: Ashkenazi, Avi		PRIOR APPLICATION NUMBER: 60/079728
		APPLICANT: Baker Kevin P.		PRIOR FILING DATE: 1998-03-27
		APPLICANT: Botstein, David		PRIOR APPLICATION NUMBER: 60/079663
		APPLICANT: Desnoyers, Luc		PRIOR FILING DATE: 1998-03-27
		APPLICANT: Eaton, Dan		PRIOR APPLICATION NUMBER: 60/079728
		APPLICANT: Ferrara, Napoleon		PRIOR FILING DATE: 1998-03-27
		APPLICANT: Filvaroff, Ellen		PRIOR APPLICATION NUMBER: 60/079786
		APPLICANT: Fong, Sherman		PRIOR FILING DATE: 1998-03-27
		APPLICANT: Gao, Wei-Qiang		PRIOR APPLICATION NUMBER: 60/079920
		APPLICANT: Gerber, Hanspeter		PRIOR FILING DATE: 1998-03-30
		APPLICANT: Gerritsen, Mary E.		PRIOR APPLICATION NUMBER: 60/079923
		APPLICANT: Goddard, Audrey		PRIOR FILING DATE: 1998-03-30
		APPLICANT: Godowski, Paul J.		PRIOR APPLICATION NUMBER: 60/080105
		APPLICANT: Grimaldi, J. Christopher		PRIOR FILING DATE: 1998-03-31
		APPLICANT: Gurney, Austin L.		PRIOR APPLICATION NUMBER: 60/080107
		APPLICANT: Hillan, Kenneth J.		PRIOR FILING DATE: 1998-03-31
		APPLICANT: Kijavlin, Ivar J.		PRIOR APPLICATION NUMBER: 60/080165
		APPLICANT: Kuo, Sophia S.		PRIOR FILING DATE: 1998-03-31
		APPLICANT: Napier, Mary A.		PRIOR APPLICATION NUMBER: 60/080194
		APPLICANT: Pan, James;		PRIOR FILING DATE: 1998-03-31
		APPLICANT: Paoni, Nicholas F.		PRIOR APPLICATION NUMBER: 60/080327
		APPLICANT: Roy, Margaret Ann		PRIOR FILING DATE: 1998-04-01
		APPLICANT: Shelton, David L.		PRIOR APPLICATION NUMBER: 60/080328
		APPLICANT: Stewart, Timothy A.		PRIOR FILING DATE: 1998-04-01
		APPLICANT: Tumas, Daniel		PRIOR APPLICATION NUMBER: 60/080333
		APPLICANT: Williams, P. Mickey		PRIOR FILING DATE: 1998-04-01
		APPLICANT: Wood, William I.		PRIOR APPLICATION NUMBER: 60/081049
		TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic		PRIOR FILING DATE: 1998-04-08
		Acids Encoding the Same		PRIOR APPLICATION NUMBER: 60/081071
		FILE REFERENCE: P2630P1C21		PRIOR FILING DATE: 1998-04-08
		CURRENT APPLICATION NUMBER: US/09/978,423A		PRIOR APPLICATION NUMBER: 60/081195
		CURRENT FILING DATE: 2002-05-16		PRIOR FILING DATE: 1998-04-08
		PRIOR APPLICATION NUMBER: 09/918585		PRIOR APPLICATION NUMBER: 60/081203
		PRIOR FILING DATE: 2001-07-30		PRIOR FILING DATE: 1998-04-09
		PRIOR APPLICATION NUMBER: 60/062250		PRIOR APPLICATION NUMBER: 60/081229
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		PRIOR APPLICATION NUMBER: 60/064249		PRIOR APPLICATION NUMBER: 60/081955
		PRIOR FILING DATE: 1997-11-03		PRIOR FILING DATE: 1998-04-15
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		PRIOR FILING DATE: 1998-03-10		PRIOR FILING DATE: 1998-04-15
		PRIOR APPLICATION NUMBER: 60/077632		PRIOR APPLICATION NUMBER: 60/082568
		PRIOR FILING DATE: 1998-03-11		PRIOR FILING DATE: 1998-04-21
		PRIOR APPLICATION NUMBER: 60/077641		PRIOR APPLICATION NUMBER: 60/082569
		PRIOR FILING DATE: 1998-03-11		PRIOR FILING DATE: 1998-04-21
		PRIOR APPLICATION NUMBER: 60/077649		PRIOR APPLICATION NUMBER: 60/082704
		PRIOR FILING DATE: 1998-03-11		PRIOR FILING DATE: 1998-04-22
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/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082700
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/ PRIOR APPLICATION NUMBER: 60/082797
/ PRIOR FILING DATE: 1998-04-22
/ PRIOR APPLICATION NUMBER: 60/082796
/ PRIOR FILING DATE: 1998-04-23
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/ PRIOR FILING DATE: 1998-04-27
/ PRIOR APPLICATION NUMBER: 60/083322
/ PRIOR FILING DATE: 1998-04-28
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/ PRIOR FILING DATE: 1998-04-29
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/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083545
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083554
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083558
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083559
/ PRIOR FILING DATE: 1998-04-29
/ PRIOR APPLICATION NUMBER: 60/083500
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/ PRIOR APPLICATION NUMBER: 60/083742
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/ PRIOR FILING DATE: 1998-05-05
/ PRIOR APPLICATION NUMBER: 60/084414
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/ PRIOR APPLICATION NUMBER: 60/084441
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/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1.19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-423A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTGGCAATCTTCACGGGGCTG 193
QY 21 AlaIleLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GCTGCTCTGTCTCTTCCAAAGGAGTGCCCGTGGCGAGGAGATGCCACCTTCCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGGACACGTGACCGGTCCGCGAGGGGAGAGCCACCCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGTCACCCGGGTGGCTGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGACGTGGATGTGTATCAGCGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACCCACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCCAAAATTTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAAAGGGGAACAATATTAGCCTCACCTGCTATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCCAGACGCTACCGTTACTTTGGAGACACATCTCTCCCAAGCGGTTGGTTGG 673
QY 181 SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
DB 674 AGTGAAGACGATATCTTGGAAATTCAGGGGCATCACCCCGGAGCAGTCAAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220
DB 734 TGCAGTGCCTCCATGACGTGGCCCGGCCGCTGGTACGGAGAGTAAGGTCAACGCTGAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
DB 794 TATCCACCATACATTTCAAGAGCCAAAGGTACAGGTGTCCTCCCGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspLys 260
DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGTCTCTGAACATGACATATGGAACATACACTTGGCGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGCTCAGCGAGGTGAC 1093
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; PRIOR APPLICATION NUMBER: 60/083336  
 ; PRIOR FILING DATE: 1998-04-27  
 ; PRIOR APPLICATION NUMBER: 60/083322  
 ; PRIOR FILING DATE: 1998-04-28  
 ; PRIOR APPLICATION NUMBER: 60/083392  
 ; PRIOR FILING DATE: 1998-04-29  
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 ; PRIOR APPLICATION NUMBER: 60/083500  
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 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 1,19e-41  
 Score: 2408.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 10  
 Length: 1679  
 Matches: 344  
 Conservatives: 0  
 Mismatches: 0  
 Indels: 0  
 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-193a-522 (1-1679)  
 QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
 DB 134 ATGAAACCATCCAGCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193  
 QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
 DB 194 GCTGCTCTGTGTCTCTTCAAGGAGTGCCTGCGGAGGAGATGCGGAGATGCCACCTTCCCCAAA 253  
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
 DB 254 GCTATGGACAACTGACCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313  
 QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80  
 DB 314 AACCGGTCACCGGGTGGCTGGCTAAACCGCAGCAGCATCTCTATGCTGGGAATGAC 373  
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100  
 DB 374 AAGTGGTCCCTGGATCCTCGCGTGTCTCTTGTGACAAACACCCAAACGAGTACAGCATC 433  
 QY 101 GluIleGlnAsnValAspValTyArgGluGlyProTyThrCysSerValGlnThrAsp 120  
 DB 434 GAGATCCAGAACGCTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493  
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553  
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
 DB 554 ATTCTTTCAGATATCTCCATTAATGAGGAGAACATATTAGCTCCTCCTGCTAGCAACT 613  
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
 DB 614 GGTAGACCAGAGCCTTACGGTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673  
 QY 181 SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrglu 200  
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAGGGGACTACGAG 733  
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValVal 220  
 DB 734 TGCAGTGGCTCCATGACGTGGCCGCGCGCTGGTACGAGAGTAAAGGTACACCGTGAAC 793  
 QY 221 TyrProTyroIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
 DB 794 TATCCACCATACATTTCAAGGCCAAGGTACAGGTGTCCCGTGGGACAAAGGGGACCA 853  
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyroIleAspAspLys 260  
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAGGATGACAAA 913  
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
 DB 914 AGACTGATTGAAGGAAAGAGGGGTGAAGTGGAAACAGACACCTTCTCTCAAAATC 973  
 QY 281 IlePhePheAsnValSerGluHisAspTyrglyAsnTyThrCysValAlaSerAsnLys 300  
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 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
 DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTGGTCCAGGCGCGCTCAGGAGGTGAGC 1093  
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 QY 341 LeuLeuLysPhe 344  
 DB |||||

Db 1154 CTTCTCAATTT 1165

RESULT 18

US-09-999-830A-522

Sequence 522, Application US/09999830A

Publication No. US2003007700A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi

APPLICANT: Baker Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnovers, Luc

APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleon

APPLICANT: Filvaroff, Ellen

APPLICANT: Fong, Sherman

APPLICANT: Gao, Wei-Qiang

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Hillan, Kenneth J.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Kuo, Sophia S.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Shelton, David L.

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2630P1C70

CURRENT APPLICATION NUMBER: US/09/999,830A

PRIOR FILING DATE: 2001-08-31

PRIOR APPLICATION NUMBER: 09/918585

PRIOR FILING DATE: 2001-07-30

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

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 ; PRIOR FILING DATE: 1998-05-15  
 ; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 1,19e-41  
 Score: 2408.00  
 Percent Similarity: 100.00%  
 Best Local Similarity: 100.00%  
 Query Match: 100.00%  
 DB: 10  
 Gaps: 0  
 Length: 1679  
 Matches: 344  
 Conservative: 0  
 Mismatches: 0  
 Indels: 0

US-10-017-084a-523 (1-344) x US-09-999-830A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
 DB 134 ATGAAACCATCCAGGCCAAATGCAATCTATCTCTGGGCAATCTTACGGGGCTG 193

QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
 DB 194 GCTGCTCTGTGTCTCTTCAAGGAGTGCCCGTGCAGCGGAGATGCCACCTTCCCCAAA 253  
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
 DB 254 GCTATGGACAACGTCAGCGTCCGGCAGGGGAGAGCGCCACCTCAGGTGCACTATTGAC 313  
 QY 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80  
 DB 314 AACCGGGTCACCCGGGTGGCTGTAAACCGCAGCAGCACCATCTCTATGCTGGGAATGAC 373  
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
 DB 374 AAGTGGTGCCTGGATCCTCGCGTGGTCTTCTGAGCAACCCCAACGCGAGTACAGATC 433  
 QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
 DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC 493  
 QY 121 AsnHisProLysThrSerArgValHisIleuIleValGlnValSerProLysIleValGlu 140  
 DB 494 AACCAACCCCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTGTAGAG 553  
 QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
 DB 554 ATTTCTTCAGATATCTCCATTAATGAGGGAACAATATTAGCCTCACCCTGATAGCAACT 613  
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
 DB 614 GGTAGACCAGAGCCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673  
 QY 181 SerGluAspGluTyrIleuGlnIleThrArgGluGlnSerGlyAspTyrGlu 200  
 DB 674 AGTGAAGACGAATACTTGGAAATTCAGGCAATCCCGGAGCAGTCACGGGACATACGAG 733  
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220  
 DB 734 TGCAGTGGCTTCAATGACGTGGCCCGCCCGTGGTACGGAGAGTAAAGTCCACCGTAAC 793  
 QY 221 TyrProTyrTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
 DB 794 TATCCACCACATACATTCAGAGCCAAAGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853  
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspLys 260  
 DB 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAAGATGACAAA 913  
 QY 261 ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
 DB 914 AGACTGATTTGAAGGAAGAAAGGGGTGAAGTGGAAACAGACCTTCTCTCAAAACTC 973  
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
 DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGGAATACACTTGGGTGGCTCCCAACAG 1033  
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValValSerGluValSer 320  
 DB 1034 CTGGGCCACCAATGCCAGCATCATGTATTGTTCAGGGCCGCTCAGCGAGGTAGC 1093  
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340  
 DB 1094 AACGGCAGCTCGCAGGAGGGCAGCTCGCTGTGGCTGTGCTTCTTCTTGTCTTGCACCTG 1153  
 QY 341 LeuLeuLysPhe 344  
 DB 1154 CTCTCAAAATTT 1165

## RESULT 19

US-09-978-757A-522  
 ; Sequence 522, Application US/09978757A  
 ; Publication No. US20030083248A1  
 ; GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi  
APPLICANT: Baker Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnovers, Luc  
APPLICANT: Eaton, Dan  
APPLICANT: Ferrara, Napoleon  
APPLICANT: Filvaroff, Ellen  
APPLICANT: Fong, Sherman  
APPLICANT: Gao, Wei-Qiang  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Hillan, Kenneth J.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Kuo, Sophia S.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James;  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Shelton, David L.  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2630PIC26  
CURRENT APPLICATION NUMBER: US/09/978,757A  
CURRENT FILING DATE: 2002-03-19  
PRIOR APPLICATION NUMBER: 09/918585  
PRIOR FILING DATE: 2001-07-30  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/064249  
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 ; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679  
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 Best Local Similarity: 100.00% Mismatches: 0  
 Query Match: 100.00% Indels: 0  
 DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-757A-522 (1-1679)

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 DB 134 ATGAAACCATCCAGCAAAATGCAATTTCTATCTCTTGGCAATCTTCACGGGGCTG 193  
 QY 21 AlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
 DB 194 GCTGCTCTGTCTCTTCCAAAGAGTGCCGTCGCGAGGGAGATGCCACCTTCCCAA 253  
 QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrIleuArgCysThrIleAsp 60  
 DB 254 GCTATGGACAACGTGACGTCGGGAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313

QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80  
 DB 314 AACCGGGTCACCGGGTGGCGCTGAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373  
 QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100  
 DB 374 AAGTGGTGGCTGGATCTCTCGGGTGGTCTCTTGAGCAACACCCAAACGAGTACAGCATC 433  
 QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTyrThrCysSerValGlnThrAsp 120  
 DB 434 GAGATCCAGAAACGTGGATGTGTATGACGAGGCGCCCTTACACCTGCTCGGTGAGACAGAC 493  
 QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
 DB 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTCAAGTATCTCCCAAAATTGTAGAG 553  
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 DB 554 ATTCTTCAGATATCTCCATTAAAGAAGGAACAATATTAGCCTCACCTGCATAGCAACT 613  
 QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
 DB 614 GGTAGACCAAGCCCTACCGTTTACTTTGGAGACACATCTCTCCAAAGCGTTGGCTTTGTG 673  
 QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
 DB 674 AGTGAAGACGAATCTTGGAAATTCAGGGCATACCCGGGAGCAGTCCAGGGGATACGAG 733  
 QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValLysValThrValAsn 220  
 DB 734 TGCAGTGCCTCCAATGACGTGCGCGCGCGTGGGTACGAGAGTAAAGSTCACCGTGAAC 793  
 QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
 DB 794 TATCCACCATATCTTTCAGAAAGCCAAAGGTTACAGGTGTCCCGCTGGGACAAAGGGGACA 853  
 QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrIleAspAspLys 260  
 DB 854 CTGCAGTGTGAAGCCCTCAGCAGTCCCTCCAGAGAAATTCAGGTGTACAGGATGACAAA 913  
 QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
 DB 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACACAGACCTTTCTCTCAAACTC 973  
 QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
 DB 974 ATCTTCTTCAATGTCTCTGAAACATGACTATGGAACTACACTTGCCTGCGCTCCCAACAG 1033  
 QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320  
 DB 1034 CTGGSCCACCACCATGCCAGCATCATGTATTTGGTCCAGGGCGCTCAGCGAGGTGAGC 1093  
 QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340  
 DB 1094 AACGGCAGCTCAGGAGGAGGAGGCTGCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1153  
 QY 341 LeuLeuLysPhe 344  
 DB 1154 CTCTCAAAATTT 1165

## RESULT 20

US-09-978-187B-522  
 ; Sequence 522, Application US/09978187B  
 ; Publication No. US20030096744A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ashkenazi, Avi  
 ; APPLICANT: Baker Kevin P.  
 ; APPLICANT: Botstein, David  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Eaton, Dan  
 ; APPLICANT: Ferrara, Napoleon  
 ; APPLICANT: Filvaroff, Ellen

; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary B.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kijavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC5  
; CURRENT APPLICATION NUMBER: US/09/978,187B  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/064249  
; PRIOR FILING DATE: 1997-11-03  
; PRIOR APPLICATION NUMBER: 60/065311  
; PRIOR FILING DATE: 1997-11-13  
; PRIOR APPLICATION NUMBER: 60/065364  
; PRIOR FILING DATE: 1997-11-21  
; PRIOR APPLICATION NUMBER: 60/077450  
; PRIOR FILING DATE: 1998-03-10  
; PRIOR APPLICATION NUMBER: 60/077632  
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; PRIOR APPLICATION NUMBER: 60/077791  
; PRIOR FILING DATE: 1998-03-12  
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; PRIOR FILING DATE: 1998-03-13  
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; PRIOR APPLICATION NUMBER: 60/078936  
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; PRIOR APPLICATION NUMBER: 60/078910  
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; PRIOR FILING DATE: 1998-03-25  
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; PRIOR FILING DATE: 1998-03-26  
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; PRIOR FILING DATE: 1998-03-30  
; PRIOR APPLICATION NUMBER: 60/080105  
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; PRIOR APPLICATION NUMBER: 60/080107  
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; PRIOR FILING DATE: 1998-03-31  
; PRIOR APPLICATION NUMBER: 60/080194  
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; PRIOR FILING DATE: 1998-04-01  
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; PRIOR FILING DATE: 1998-04-15  
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; PRIOR APPLICATION NUMBER: 60/081952  
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; PRIOR APPLICATION NUMBER: 60/082797  
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; PRIOR APPLICATION NUMBER: 60/082796  
; PRIOR FILING DATE: 1998-04-23  
; PRIOR APPLICATION NUMBER: 60/083336  
; PRIOR FILING DATE: 1998-04-27  
; PRIOR APPLICATION NUMBER: 60/083322  
; PRIOR FILING DATE: 1998-04-28  
; PRIOR APPLICATION NUMBER: 60/083392  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083495  
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; PRIOR APPLICATION NUMBER: 60/083545  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083554  
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; PRIOR APPLICATION NUMBER: 60/083558  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083559  
; PRIOR FILING DATE: 1998-04-29  
; PRIOR APPLICATION NUMBER: 60/083500



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; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083742
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084598
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084600
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
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; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085689
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1,19e-41
Score: 2408.00
Length: 1679
Percent Similarity: 100.00%
Matches: 344
Best Local Similarity: 100.00%
Conservative: 0
Mismatches: 0
Query Match: 100.00%
Indels: 0
DB: 10
Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-187B-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
DB 134 ATGAAACCATCCAGCAAAATGCAATTTCTATCTTGGCAATCTTCACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
DB 194 GTGTCTGTCTCTTCAAGAGAGTCCCGCGCAGCGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
DB 254 GCTATGACACACTGACGTCCCGCAGGGGAGAGCCACCTCAGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTrpAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCACCATCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100

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DB 374 AAGTGGTGGATCCTCGCGTGGTCTCTCTGAGCAACACCCCAACGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyraaspGluGlyProTyThrCysSerValGlnThrAsp 120
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGCCCTTACACCTGCTCGGTGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
DB 494 AACACCCCAAGACCTCTAGGGTCCACTCTATTGCGAAGTATCTCCCAAAATTGTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGAACAATATTAGCTCACCCTGCATAGCAACT 613
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
DB 614 GGTAGACCAGACCTTACCGGTACTTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyTrpLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyTrp 200
DB 674 AGTGAAGACGAATACTTGGAAATTCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACGAG 733
QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgValValValValValValAsn 220
DB 734 TGCAGTGGCTCCCAATGACGTGGCGCCGCGGTGTACGAGAGTAAAGGTCAACCGTGAAC 793
QY 221 TyTrpProTyTrpIleSerGluAlaGlyGlyThrGlyValProValGlyGlyGlyThr 240
DB 794 TATCCACCATACATTTCAAGAGCCAAAGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyTrpLysAspLys 260
DB 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
DB 914 AGACTGATTGAAGGAAGAAAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
QY 281 IlePhePheAsnValSerGluHisAspTyTrpGlyAsnTyThrCysValAlaSerAsnLys 300
DB 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACACTACACTTGGTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
DB 1034 CTGGGCCACACCAATGCCAGCATCATGTATTTGTCAGCGCGCGTCCAGCGAGTGCAGC 1093
QY 321 AsnGlyThrSerArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
DB 1094 AACGGCACGTGAGGAGGGCAGGCTGCTGTGGTGTCTGTGGTGTCTGTGGTGTCTGTGGTGT 1153
QY 341 LeuLeuLysPhe 344
DB 1154 CTCTCAAAATTT 1165

RESULT 21
US-09-978-643A-522
; Sequence 522, Application US/09978643A
; Publication No. US20030104998A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher

```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C16
; CURRENT APPLICATION NUMBER: US/09/978,643A
; CURRENT FILING DATE: 2001-10-16
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-978-643A-522

Alignment Scores:
Pred. No.: 1,19e-41 Length: 1679
Score: 2488.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084a-523 (1-344) x US-09-978-643A-522 (1-1679)

Qy 1 MetLysThrLeuGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAAACCACTCCAGCCAAATGCAATCTCTCTTGGGCAATCTTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGGAGTCCCGTGGCGAGCGAGATGCCACCTTCCCCAAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyCysLeuSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACAAACGTCGCGTCCGCGAGGGGAGAGCCACCTCAGTGCATATTGAC 313
Qy 61 AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80
Db 314 AACCGGTGTCACCGGGTGGCTGTAAACCGCAGCACCATCTCTTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTGCTGGATCTCTCGCTGGTCTTCTGAGCAACACCCAAACGCGATCAGATC 433
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTCGATGTATGACGAGGGCCCTTACACCTCTCGTGGCAGACAGAC 493
Qy 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCAACCAAGACCTCTAGGGTCCACTCTATTGTGCAAGATATCTCCCAAAATGTAGAG 553
Qy 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTTCTTCAGATATCTCCATTAATGAAGGGGAACATATTAGCCTCAGCTGCTAGCAACT 613
Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGACCTTACGTTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200

; 674 AGTGAAGACGATACTTGGAAATTCAGGSCATCACCAGGAGCAGTCAAGGAGCTACGAG 733
; 201 CysSerAlaSerAsnAspValAlaProValValArgValArgValValValValValAsn 220
; 734 TGCAGTGCCTCCAATGACGTGGCGGCGCGGTGTACGGAGAGTAAAGGTCAACCGTGAAC 793
; 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
; 794 TATCCACCATACATTTCAAGAGCCAGGGTACAGGTGTCCCGTGGGACAAAGGGGACA 853
; 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
; 854 CTGCAGTGTGAAGCCTCAGCAGTCCCTCAGCAGATTCCTGAGGATGACAA 913
; 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
; 914 AGACTGATTTGAAGGAAAGAGGGGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 973
; 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
; 974 ATCTTCTTCAATGTCTCTGAACATGACTATGGAACACTACACTTGCCTGCTCCCAACAG 1033
; 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320
; 1034 CTGGGCCACCAATGCCAGCATCATGCTATTGTTGGTCCAGGCGCGTCAAGCGAGGTGAGC 1093
; 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValLeuHisLeu 340
; 1094 AACGGCACCTCGAGGAGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1153
; 341 LeuLeuLysPhe 344
; 1154 CTTCACAAATTT 1165

RESULT 22
US-09-978-375A-522
; Sequence 522, Application US/09978375A
; Publication No. US20030130181A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kijavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630P1C24
; CURRENT APPLICATION NUMBER: US/09/978,375A
; CURRENT FILING DATE: 2002-04-19
; Prior Application removed - See File Wrapper or Palm
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; NUMBER OF SEQ ID NOS: 624  
; SEQ ID NO 522  
; LENGTH: 1679  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-978-375A-522

## Alignment Scores:

Pred. No.: 1 19e-41 Length: 1679  
Score: 2408.00 Matches: 344  
Percent Similarity: 100.00% Conservativity: 0  
Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-375A-522 (1-1679)

QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20  
DB 134 ATGAAACCATCCAGCCAAAATGCAATTCATCTCTGGCAATCTTCACGGGGCTG 193  
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40  
DB 194 GCTGCTCTGTGCTCTTCCAAAGAGTGCCTGCGCAGCGGAGATGCCACCTTCGCCAAA 253  
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60  
DB 254 GCTATGGACAACTGACGGTCCGGCAGGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313  
QY 61 AsnArgValThrArgValAlaIleTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp 80  
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCCGACGACCATCTCTATCTGGGAATGAC 373  
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTrpSerIle 100  
DB 374 AAGTGGTGCCTGGATCCTCGCTGGTCTCTTGAGCAACCCCAACGCGTACGACATC 433  
QY 101 GluIleGlnAsnValAspValTrpAspGluGlyProTyThrCysSerValGlnThrAsp 120  
DB 434 GAGATCCAGAACGTGGATGTGTATGACGAGGGGCCCTTACACCTGCTCGGTGCAGACAG 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
DB 494 AACCCACCCAAAGACCTTAGGTGTCACCTCATTTGTGCAAGTATCTCCCAAAATTTAGAG 553  
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
DB 554 ATTTCTTCAGATATCTCCATTAATGAGGAGACATATTAGCTCACCTGCATAGCACT 613  
QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
DB 614 GGTAGACCAAGACCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673  
QY 181 SerGluAspGluTyLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTrpGlu 200  
DB 674 AGTGAAGACGAATCTTGAATATTCAGGCGCATCACCGGAGCAGTCAGGGGACTACGAG 733  
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValLysValThrValAsn 220  
DB 734 TGCAGTGCCTCCATGACGTGGCGGCGCGGTGTGTACGAGAGTAAGTCCACCGTGAC 793  
QY 221 TyrProTyTrpIleSerGluAlaLysGlyThrGlyValProValGlnLysGlyThr 240  
DB 794 TATCCACCATATCTTCAAGCAAGGTCAGGTGTCCCGTGGGCAAAAGGGGACA 853  
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyTrpAspAspLys 260  
DB 854 CTGCACTGTGAAGCTTCAGCAGTCCCTCAGCAGATTCAGTGTGTACAGGATGACAAA 913  
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
DB 914 AGACTGATTGAAGAAAGAGGGTGAAGTGAAGAAAGACACCTTCTCTCAAAACTC 973

## RESULT 23

US-09-978-298A-522

; Sequence 522, Application US/09978298A

; Publication No. US20030134785A1

; GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James;  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C2  
; CURRENT APPLICATION NUMBER: US/09/978,298A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR FILING DATE: 1998-03-12

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QY 321 AsnGlyThrSerArgArgAlaGlyCysValTrpLeuProLeuValLeuHisLeu 340  
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DB 1154 CTTCTCAAAATTT 1165

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## Alignment Scores:

Pred. No.: 1,19e-41 Length: 1679  
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Best Local Similarity: 100.00% Mismatches: 0  
Query Match: 100.00% Indels: 0  
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US-10-017-084A-523 (1-344) x US-09-978-298A-522 (1-1679)

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DB 194 GTGTCTCTGTCTCTTCCAGAGTGCCTGCGGAGCGGAGATGCCACCTTCCCAAA 253
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DB 254 GCTATGGACAACTGACGCTCCGGCAGGGGAGAGCGCCACCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaThrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
DB 314 AACCGGGTCACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
DB 374 AGTGGTGCTGGATCTCGGTGCTCTTCTGAGCAACACCCAGCAGTACGATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
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QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
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## RESULT 24

US-09-978-188A-522  
; Sequence 522, Application US/09978188A  
; Publication No. US20030139328A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
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; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630PIC8  
; CURRENT APPLICATION NUMBER: US/09/978,188A  
; CURRENT FILING DATE: 2001-10-15  
; PRIOR APPLICATION NUMBER: 09/918585  
; PRIOR FILING DATE: 2001-07-30  
; PRIOR APPLICATION NUMBER: 60/062250  
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US-10-017-084A-523 (1-344) x US-09-978-188A-522 (1-1679)

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QY 41 AlaMetAspAsnValThrValArgGlnGlySerAlaThrLeuArgCysThrIleAsp 60  
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Db 314 RACCGGGTCACCCGGGTGGCTGGCTGTAACCGCAGCACCATCTCTATCTGGGAATGAC 373  
QY 81 LysTyrCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100  
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Db 434 GAGATCCAGACGTGGATGTGTATGACGAGGGCCCTTACACCTCTGCTCGGTGCAGACAGAC 493  
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140  
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QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160  
Db 554 ATTCTTTCAGATATCTCCATTAATGAAGGAAACAATATTAGCTCACCTGCATAGCACT 613  
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QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200  
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QY 201 CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220  
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QY 221 TyrProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
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QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyValAlaValSerGluValSer 320  
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QY 321 AsnGlyThrSerArgAlaGlyCysValTyrLeuLeuProLeuLeuValLeuHisLeu 340  
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QY 341 LeuLeuLysPhe 344  
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## RESULT 25

US-09-978-681A-522  
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; Publication No. US20030195148A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
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; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2630P1C18  
; CURRENT APPLICATION NUMBER: US/09/978,681A  
; CURRENT FILING DATE: 2002-03-19  
; PRIOR APPLICATION NUMBER: 09/918585  
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; PRIOR APPLICATION NUMBER: 60/085697

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Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-681A-522 (1-1679)

Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrrAlaIlePheThrGlyLeu 20

Db 134 ATGAACCATCCAGCAAAATGCAATTCATTCTTTGGCAATCTTCACGGGCTG 193



QY		21	AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db		194	GCTGCTGTGTGTTCTTCCAAAGAGTGCCCGTCGCAGCGAGATGCCACTTCCCAAAA	253
QY		41	AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp	60
Db		254	GCTATGGACAACTGAGCGTCCGGCAGCGGGGAGAGCGCCACCTTCAGGTGCATATTGAC	313
QY		61	AsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyAlaGlyAsnAsp	80
Db		314	AACCGGGTCAACCGGGTGGCTGGCTAAACCAGCACCATCTCTATGTCGGGAATGAC	373
QY		81	LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle	100
Db		374	AAGTGGTGCCCTGGATCTCCGGTGGTCTCTCAGACNACCCCNAACGAGTAACGATC	433
QY		101	GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp	120
Db		434	GAGATCCAGAACGTGGATGTATGACAGAGGGCCCTTACACCTGCTCGGTGCAGACAGAC	493
QY		121	AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu	140
Db		494	AACCAACCCAAAGACCTCTAGGGTCCACTCATTTGTGCAGATATCTCCCAAATGTAGAG	553
QY		141	IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr	160
Db		554	ATTTCITTCAGATATCTCATTAATGAAGGAAACAATAATTAGCCCTCACCTGCATAGCAACT	613
QY		161	GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal	180
Db		614	GGTAGACCAGCGCTACGGTTACTTGGAGACACATCTCTCCCAAGCGGTGGCTTTGGT	673
QY		181	SerGluAspGluTyrIleuGluIleGlnGlyIleThrArgGluInSerGlyAspTyrGlu	200
Db		674	AGTGAAGACAAATACTTTGAAAAITCAGGGCATCACCCGGGAGCAGTCAAGGGGACTACGAG	733
QY		201	CysSerAlaSerAsnAspValAlaAlaProValValArgArgVallysValThrValAsn	220
Db		734	TGCAGTGCCTCCAATGACGTGGCGCGCCCGTGGTACGGAGATTAAGGTCACCGTGAAC	793
QY		221	TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr	240
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QY		241	LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys	260
Db		854	CTGCAGTGTGAAGCCTCAGCAGTCCCCCTCAGCAGANTCCAGTGTACAAGGATGACAAA	913
QY		261	ArgLeuIleGluGlyLysLysGlyValLysValGluAsnArgPropheLeuSerLysLeu	280
Db		914	AGACTATTGAAGGAAAGAAAGGGGTGAAAGTGGAAAACAGACCTTTCTCTCAAAATC	973
QY		281	IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys	300
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QY		301	LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer	320
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QY		321	AsnGlyThrSerArgArgAlaGlyCysValTrpLeuLeuProLeuLeuValIleHisLeu	340
Db		1094	AACGGCAGTCCGAGAGGGCAGGCTGGCTCTGGCTGTCTCTCTCTCTCTCTCTCTCTCT	1153
QY		341	LeuLeuLysPhe	344
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RESULT 26

US-09-978-194A-522

US-09-378-194A-522  
; Sequence 522, Application US/09978194A

; Publication No. US20030195333A1

; GENERAL INFORMATION:

/ APPLICANT: Ashkenazi, Avi  
 / APPLICANT: Baker Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan  
 / APPLICANT: Ferrara, Napoleon  
 / APPLICANT: Filvaroff, Ellen  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gao, Wei-Qiang  
 / APPLICANT: Gerber, Hanspeter  
 / APPLICANT: Gerritsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Hillan, Kenneth J.  
 / APPLICANT: Kljavin, Ivar J.  
 / APPLICANT: Kuo, Sophia S.  
 / APPLICANT: Napier, Mary A.  
 / APPLICANT: Pan, James;  
 / APPLICANT: Paoni, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Shelton, David L.  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumaas, Daniel  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 / FILE OF INVENTION: Acids Encoding the Same  
 / FILE REFERENCE: P2630PIC10  
 / CURRENT APPLICATION NUMBER: US/09/978,194A  
 / CURRENT FILING DATE: 2001-10-15  
 / PRIOR APPLICATION NUMBER: 09/918585  
 / PRIOR FILING DATE: 2001-07-30  
 / PRIOR APPLICATION NUMBER: 60/062250  
 / PRIOR FILING DATE: 1997-10-17  
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;; PRIOR APPLICATION NUMBER: 60/085573  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085704  
;; PRIOR FILING DATE: 1998-05-15  
;; PRIOR APPLICATION NUMBER: 60/085697

## Alignment Scores:

Pred. No.:	1.19e-41	Length:	1679
Score:	2408.00	Matches:	344
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	10	Gaps:	0

US-10-017-084A-523 (1-344) x US-09-978-194A-522 (1-1679)

Qy	1	MetLysThrIleGlnProLysMetHisnSerIleSerTrpAlaIlePheThrGlyLeu	20
Db	134	ATGAACCATCCAGCCAAAATGCACAAATCTCTTGGGCAATCTTTCACGGGCGTG	193
Qy	21	AlaIleLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys	40
Db	194	GCTGCTGTGTCTCTTCCAGGAGTCCCGTGCGCAGCGAGATGCCACCTTCCCAAA	253
Qy	41	AlaMetAspIleValThrValArgGlnGlyCyluSerAlaThrLeuArgCysThrIleAsp	60
Db	254	GCTATGGACAAACGTGACGCTCCCGCAGGGGAGAGCCGCCCTCAGTGCTATTGAC	313

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QY 61 AsnArgValThrArgValAlaTrrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGACACCGGGTGGCTGGCTAAACCGCAGCACCATTCTCTATCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerile 100
Db 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTCGATGTATGATGAGGCGCCCTTACACCTGCTCGGTGCGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCACCCAAAGACCTTAGGGTCCACCTATTGCAAGATATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
Db 554 ATTCTCTCAGATATCTCCATTAATGAAGGAAACAATATTAGCCTCACCTGCATAGCACT 613
QY 161 GlyArgProGluProThrValThrTrrArgHisIleSerProLysAlaValGlyPheVal 180
Db 614 GGTAGACCAAGAGCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTGGCTTTGTG 673
QY 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
Db 674 AGTGAAGAGCATACTTGGAAATTCAGGGCATCCCGGAGCAGTCAAGGAGTACAGAG 733
QY 201 CysSerAlaSerAsnAspValAlaProValValArgValLysValThrValAsn 220
Db 734 TGCAGTGGCTCAATGACGTGGCGCGCCGCTGTACGAGAGTAAAGGTCAACCGTGAAC 793
QY 221 TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240
Db 794 TATCCACCATACATTTTCAAGAGCAAGGGTACAGGTGTCCCGGTGGGACAAAGGGGACA 853
QY 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrrTyrLysAspAspLys 260
Db 854 CTGCAGTGTGAAGCTCAGCAGTCCCTCAGCAGAAATTCAGTGTGTACAGGATGACAA 913
QY 261 ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280
Db 914 AGACTGATTCAAGGAAAGAAAGGGGTGAAAGTGGAAACACAGACCTTTCTCTCAAACTC 973
QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
Db 974 AICTTCTTCAATGTCTCTGAACATGACTATGGAACTACACTTGGCTGGCTCCCAACAG 1033
QY 301 LeuGlyHisThrAsnAlaSerIleMetLeuPheGlyProGlyAlaValSerGluValSer 320
Db 1034 CTGGGCCACACCAATGCCAGCATCATGCTATTGGTCCAGGCGCGTCAAGGAGGTGAGC 1093
QY 321 AsnGlyThrSerArgArgLaglyCysValTrrLeuLeuProLeuValLeuHisLeu 340
Db 1094 AACGGCACGTGAGGAGGAGCGTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTG 1153
QY 341 LeuLeuLysPhe 344
Db 1154 CTTCTCAAAATTT 1165

RESULT 27
US-09-999-829A-522
; Sequence 522, Application US/09999829A
; Publication No. US20030195344A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Kuo, Sophia S.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James.
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PIC61
; CURRENT APPLICATION NUMBER: US/09/999,829A
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 624
; Prior Application removed - See File Wrapper or Palm
; SEQ ID NO 522
; LENGTH: 1679
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-999-829A-522

Alignment Scores:
Pred. No.: 1,19e-41 Length: 1679
Score: 2408.00 Matches: 344
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-10-017-084A-523 (1-344) x US-09-999-829A-522 (1-1679)
QY 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAATAACCATCCACCCAAAATGCAAAATCTATCTCTTGGGCAATCTTACGGGGCTG 193
QY 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTGTCTCTTCCAGGAGTGGCCGTCGCGAGGAGATGCCACCTTCCCAAA 253
QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGGCAACCGTACCGTCCGGCAGGGGAGAGCGCCACCCCTCAGGTGCATATTGAC 313
QY 61 AsnArgValThrArgValAlaTrrLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGCTCACCGGGTGGCTGGCTTAAACCGCAGCACCATTCTCTATGCTGGGAATGAC 373
QY 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerile 100
Db 374 AAGTGGTGGCTGGATCTCGGTGGTCTCTGAGCAACACCCAAACGCGAGTACAGCATC 433
QY 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGACGTCGATGTATGATGAGGCGCCCTTACACCTGCTCGGTGCGAGACAGAC 493
QY 121 AsnHisProLysThrSerArgValHisLeuIleValGlnValSerProLysIleValGlu 140
Db 494 AACCACCCAAAGACCTTAGGGTCCACCTATTGCAAGATATCTCCCAAAATTTAGAG 553
QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnAsnIleSerLeuThrCysIleAlaThr 160
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Db 554 ATTCTTCAGATATCTCCATTAAATGAAGGGAACAAATATTAGCCTCACCTGCATAGCAACT 613  
QY GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180  
Db 614 GGTAGACAGAGCCCTACGGTTACTTGGAGACACATCTCTCCAAAGCGGTTGGCTTTGTG 673  
QY SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGlnSerGlyAspTyrGlu 200  
Db 674 AGTGAAGACGAAATCTTGGAAATTCAGGGCATCACCGGGAGCAGTCAGGGGACTACAG 733  
QY CysSerAlaSerAsnAspValAlaAlaProValValArgArgValLysValThrValAsn 220  
Db 734 TGCACTGCCTCCAAATGACGTGGCCGCGCCGCTGGTACGAGAGTAAGGTACCGTGAAC 793  
QY TyrProProTyrIleSerGluAlaLysGlyThrGlyValProValGlyGlnLysGlyThr 240  
Db 794 TATCACCATATATTTCAAGACCAAGGGTACAGGTGTCCCGGTGGGACAAAAGGGGACA 853  
QY LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTyrTyrLysAspLys 260  
Db 854 CTGACGTGTGAAGCCTCAGCAGTCCCTCAGCAGAAATTCAGTGGTACAAGATGACAAA 913  
QY ArgLeuIleGluGlyLysGlyValLysValGluAsnArgProPheLeuSerLysLeu 280  
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QY IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300  
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## RESULT 28

US-09-978-299A-522

; Sequence 522, Application US/09978299A

; Publication No. US20030199435A1

## GENERAL INFORMATION:

; APPLICANT: Ashkenazi, Avi  
; APPLICANT: Baker Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan  
; APPLICANT: Ferrara, Napoleon  
; APPLICANT: Filvaroff, Ellen  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gao, Wei-Qiang  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Hillan, Kenneth J.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Kuo, Sophia S.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Shelton, David L.  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE OF INVENTION: Acids Encoding the Same  
; FILE REFERENCE: P2630P1C3  
; CURRENT APPLICATION NUMBER: US/09/978,299A  
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.: 1.19e-41
Score: 2408.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 10
Length: 1679
Matches: 344
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

US-10-017-084A-523 (1-344) x US-09-978-299A-522 (1-1679)
Qy 1 MetLysThrIleGlnProLysMetHisAsnSerIleSerTrpAlaIlePheThrGlyLeu 20
Db 134 ATGAATACCATCCAGCCAAATGCAATTCATCTCTGGCAATCTTCACGGGGCTG 193
Qy 21 AlaAlaLeuCysLeuPheGlnGlyValProValArgSerGlyAspAlaThrPheProLys 40
Db 194 GCTGCTCTGTCTCTTCCAAAGAGAGTGCCTGGCGAGGAGATGCCACCTTCCCAA 253
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
Db 254 GCTATGACACACGTCAGCGTCCGCGAGGGAGAGCCGCCCTCAGTGCACCTATTGAC 313
Qy 61 AsnArgValThrArgValAlaAlaTrpLeuAsnArgSerThrIleLeuTyrAlaGlyAsnAsp 80
Db 314 AACCGGGTCAACCGGGTGGCTGGCTAAACCGCAGCACCATCTCTATGCTGGGAATGAC 373
Qy 81 LysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThrGlnTyrSerIle 100
Db 374 AAGTGGTCCCTGGATCTCGCGTGGTCTTCTTGAGCAACACCCCAACGCGATACAGCATC 433
Qy 101 GluIleGlnAsnValAspValTyrAspGluGlyProTyrThrCysSerValGlnThrAsp 120
Db 434 GAGATCCAGAACGTCGATGTATGACGAGGGCCCTTACACCTCTCGTGCACAGACAGAC 493
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Qy 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180
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Qy 181 SerGluAspGluTyrLeuGluIleGlnGlyIleThrArgGluGlnSerGlyAspTyrGlu 200
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/ PRIOR APPLICATION NUMBER: 60/085689
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085579
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/ PRIOR APPLICATION NUMBER: 60/085580
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/ PRIOR APPLICATION NUMBER: 60/085573
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085704
/ PRIOR FILING DATE: 1998-05-15
/ PRIOR APPLICATION NUMBER: 60/085697
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Alignment Scores:

Pred. No.:	1-19e-41	Length:	1679
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US-10-017-084A-523 (1-344) x US-09-978-544A-522 (1-1679)

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QY 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60

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Db 494 AACCAACCAAGACCTCTAGGGTCCACCTCATTTGTGAAGTATCTCCCAAAATTTAGAG 553

QY 141 IleSerSerAspIleSerIleAsnGluGlyAsnIleSerLeuThrCysIleAlaThr 160

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QY 161 GlyArgProGluProThrValThrTrpArgHisIleSerProLysAlaValGlyPheVal 180

Db 614 GGTAGACCAGACCTACGGTTACTTTGGAGACACATCTCTCCAAAGCGGTGGTTTGTG 673

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; PRIOR APPLICATION NUMBER: 60/085689
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; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085704
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085697

Alignment Scores:
Pred. No.:      1,19e-41      Length:      1679
Score:          2408.00      Matches:      344
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      100.00%      Indels:      0
DB:              10          Gaps:      0

US-10-017-084A-523 (1-344) x US-09-978-665A-522 (1-1679)

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Qy 241 LeuGlnCysGluAlaSerAlaValProSerAlaGluPheGlnTrpTyrLysAspAspLys 260
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QY 914 AGACTGATTGAAGGAAAGAAAGGGGTGAAAGTGGAAACAGACCTTTCTCTCAAAACTC 973
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QY 281 IlePhePheAsnValSerGluHisAspTyrGlyAsnTyrThrCysValAlaSerAsnLys 300
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Db |||||
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Db |||||
QY 341 LeuLeuLysPhe 344
Db |||||
QY 1154 CTTCTCAAAATT 1165
Db |||||
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Search completed: May 28, 2004, 15:28:57  
Job time : 624 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 28, 2004, 12:59:14 ; Search time 3099 Seconds  
(without alignments)  
3314.808 Million cell updates/sec

Title: US-10-017-084a-523

Perfect score: 2408

Sequence: 1 MKTIQPMHNSISWAIFTGL.....RRAGCVMLPLLVHLLKPF 344

Scoring table:

BLOSUM30  
Xgapop 1.0 , Xgapext 0.1  
Ygapop 1.0 , Ygapext 0.1  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO.spool/US10017084/runat\_28052004\_125907\_29900/app\_query.fasta\_1.519  
-DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPEL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum30 -TRANS=human40.cdi -LIST=100  
-DOALIGN=200 -THR\_SCORE=ptc -THR\_MAX=100 -THR\_MIN=0 -ALIGN=30 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10017084 @CNG 1 1 3437 @runat\_28052004\_125907\_29900 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBIOCK=100 -LONGLOG  
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=1 -XGAPEXT=0.1 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=1 -YGAPEXT=0.1 -DELOP=6 -DELEXT=7

Database :

EST.\*

1: em estba.\*

2: em esthum.\*

3: em estin.\*

4: em estmu.\*

5: em estov.\*

6: em estpl.\*

7: em estro.\*

8: em htc.\*

9: gb est1.\*

10: gb est2.\*

11: gb htc.\*

12: gb est3.\*

13: gb est4.\*

14: gb est5.\*

15: em estfun.\*

16: em estom.\*

17: em gss hum.\*

18: em gss inv.\*

19: em gss pin.\*

20: em gss vrt.\*

21: em gss fun.\*

22: em gss man.\*

23: em gss mus.\*

24: em gss pro.\*

25: em gss rod.\*

26: em gss phg.\*

27: em gss vrl.\*

28: gb gss1.\*

29: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2369	98.4	1808	11	AK045973	Mus muscu
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3	2023	84.0	874	29	AY406347	Homo sapi
4	1996	82.9	874	29	AY406349	Homo sapi
5	1863	77.4	1039	10	BE798585	Mus muscu
6	1798	74.7	3166	11	AK042854	Mus muscu
7	1784	74.1	773	29	AY406348	Pan trogl
8	1736	72.1	856	13	BUI55617	AGENCOURT
9	1720	71.4	765	14	CD354474	UI-M-GMO-
10	1714	71.2	11493	29	AY404090	Mus muscu
11	1696	70.5	2798	11	AK028345	Mus muscu
12	1693	70.3	11490	29	AY404088	Homo sapi
13	1691	70.3	8928	11	AK090134	Mus muscu
14	1688	70.1	12485	29	AY404418	Homo sapi
15	1684	69.9	14278	11	AY318958	Rattus no
16	1684	69.9	14278	11	AY321317	Rattus no
17	1683	69.9	8259	11	BC038478	Mus muscu
18	1682	69.9	12304	29	AY404420	Mus muscu
19	1679	69.7	14278	11	AY318958	Rattus no
20	1679	69.7	14278	11	AY321317	Rattus no
21	1676	69.6	10481	11	AK090138	Mus muscu
22	1675	69.6	10481	11	AK090138	Mus muscu
23	1672	69.5	9744	29	AY405009	Homo sapi
24	1671	69.4	8315	11	AK090135	Mus muscu
25	1670	69.4	22715	28	AQ839851	69115-C79
26	1667	69.3	14771	28	AQ839854	260113-C5
27	1665	69.2	10560	28	AQ839853	260113-C5
28	1665	69.2	12485	29	AY404419	Pan trogl
29	1665	69.2	9567	29	AY405011	Mus muscu
30	1662	69.0	11490	29	AY404089	Pan trogl
31	1661	69.0	8928	11	AK090134	Mus muscu
32	1661	69.0	11493	29	AY404090	Mus muscu
33	1660	69.0	7866	29	AY417659	Mus muscu
34	1660	68.9	15970	28	AQ839852	260113-C5
35	1660	68.9	10638	28	AQ839855	69115-C78
36	1659	68.9	8329	11	AK090130	Mus muscu
37	1659	68.9	12349	11	AK090125	Mus muscu
38	1659	68.9	22715	28	AQ839851	69115-C79
39	1659	68.9	12349	11	AK090125	Mus muscu
40	1657	68.8	14771	28	AQ839854	260113-C5
41	1654	68.7	9097	29	AY400949	Mus muscu
42	1651	68.6	8329	11	AK090130	Mus muscu
43	1651	68.6	6468	29	AY400046	Mus muscu
44	1650	68.5	6972	29	AY405714	Homo sapi
45	1649	68.5	6468	29	AY400044	Homo sapi
46	1648	68.5	9184	29	AY402246	Homo sapi
47	1647	68.4	7518	11	BC058249	Mus muscu
48	1647	68.4	8936	11	AK090121	Mus muscu
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51	1646	68.4	15970	28	AQ839852	260113-C5
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54	1644	68.3	8373	11	BC051010	Mus muscu
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58	1639	68.1	9330	11	AK090118	Mus muscu
59	1638	68.1	8532	29	AY417357	Homo sapi
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C	71	1630.9	67.7	7134	11	AY325252	Rattus no
	72	1630.9	67.7	11487	29	AY418620	Homo sapi
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	74	1630.7	67.7	6852	11	AK090117	Mus muscu
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	76	1629.5	67.7	12304	29	AY404420	Mus muscu
C	77	1628.9	67.6	9183	29	AY400947	Homo sapi
	78	1628.6	67.6	7964	29	AY416951	Mus muscu
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C	85	1626.8	67.6	11415	29	AY418622	Mus muscu
	86	1624.2	67.5	7884	29	AY417657	Homo sapi
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C	89	1622.4	67.4	8175	11	AK090120	Mus muscu
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C	91	1621.9	67.4	8293	11	AK090126	Mus muscu
	92	1620.9	67.3	7763	11	BC047348	Mus muscu
C	93	1620.8	67.3	6921	28	AF101618	AF101618
	94	1620.2	67.3	9835	11	AK090131	Mus muscu
C	95	1619.8	67.3	7232	11	AF034176	AF034176
	96	1619.3	67.2	6966	11	AY383712	Rattus no
C	97	1618.9	67.2	11490	29	AY404089	Fan trogl
	98	1618.2	67.2	8268	11	AK090127	Mus muscu
C	99	1617.9	67.2	8284	11	AK090128	Mus muscu
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## ALIGNMENTS

RESULT 1	AK045973	1808 bp	mus musculus adult male	HTC 20-SEP-2003
LOCUS	AK045973	1808 bp	mus musculus adult male	HTC 20-SEP-2003
DEFINITION	full-length enriched library, clone:B30328N06 product:NEUROTRIMIN PRECURSOR (GP65) homolog [Rattus norvegicus], full insert sequence.			
ACCESSION	AK045973			
VERSION	AK045973.1	GI:26337738		
KEYWORDS	HTC; CAP trapper.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.			
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes			
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)			
MEDLINE	20499374			
PUBMED	11042159			
REFERENCE	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,			

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multipillar sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
PUBMED 11076861

THE RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

THE FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tanaka, T., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.go.jp/  
URL: http://phantom.gsc.riken.go.jp/  
Location/Qualifiers

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## FEATURES

source

## CDS



Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Oheato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I., Sogabe, Y., Tgami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

# TITLE JOURNAL

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, Yokohama, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/  
URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

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## ORIGIN

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US-10-017-084A-523 (1-344) x AK046377 (1-1808)

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Db 264 GCGGCTCTGTGCTCTTCCAGAGATGCGCGTGGTACGGAGATGCCACCTTTCCAAA 323
Qy 41 AlaMetAspAsnValThrValArgGlnGlyGluSerAlaThrLeuArgCysThrIleAsp 60
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SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE
AUTHORS
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
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AY406349
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Mus musculus HCM2527 gene, VIRTUAL TRANSCRIPT, partial sequence,
Genomic survey sequence.
ACCESSION
AY406349
VERSION
AY406349.1 GI:39762323
KEYWORDS
GSS.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 874)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
FEATURES
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ORIGIN
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Score: 1996.80 Matches: 282
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Best Local Similarity: 97.24% Mismatches: 2
Query Match: 82.92% Indels: 2
DB: 29 Gaps: 1

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US-10-017-084A-523 (1-344) x AY406349 (1-874)

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QY 57 CysThrIleAspAsnArgValThrArgValAlaTrpLeuAsnArgSerThrIleLeuTyr 76
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QY 77 AlaGlyAsnAspLysTrpCysLeuAspProArgValValLeuLeuSerAsnThrGlnThr 96
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# REFERENCE AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Contact: Robert Strausberg, Ph.D. Email: cgaabs-r@mail.nih.gov Tissue Procurement: DCTD/DTp cDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov Plate: L1CM779 row: d column: 04 High quality sequence stop: 849.

## FEATURES source

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## ORIGIN

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Alignment Scores:
Pred. No.: 6.57e-21 Length: 1039
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US-10-017-084A-523 (1-344) x BE798585 (1-1039)
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 1  
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 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itch, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new genes  
 Genome Res. 10 (10), 1617-1630 (2000)  
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 MEDLINE  
 PUBMED 11042159  
 3

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P.,  
 Konno, H., Akiyama, J., Nishi, K., Kikunai, T., Tashiro, H., Itoh, M.,  
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,  
 Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
 Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,  
 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,  
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer  
 Genome Res. 10 (11), 1757-1771 (2000)  
 20530913  
 MEDLINE  
 PUBMED 11076861  
 4

The RIKEN Genome Exploration Research Group Phase II Team and the  
 PANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection  
 Nature 409, 685-690 (2001)

5 The PANTOM Consortium and the RIKEN Genome Exploration Research  
 Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)

6 (bases 1 to 3166)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
 Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
 Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
 Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
 Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
 Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
 Nakamura, M., Nishi, K., Nomura, K., Nomura, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.  
 Direct Submission

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
 RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
 Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.go.jp/

URL: http://fantom.gsc.riken.go.jp/.

## FEATURES

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## ORIGIN

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Percent Similarity: 31.83% Conservative: 49  
Best Local Similarity: 26.80% Mismatches: 17  
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US-10-017-084A-523 (1-344) x AK042854 (1-3166)

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VERSION AY406348.1 GI:39762322
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SOURCE Pan troglodytes (chimpanzee)

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1 (bases 1 to 773)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL Gene trios
PUBMED Science 302 (5652), 1960-1963 (2003)
REFERENCE 14671302
AUTHORS 2 (bases 1 to 773)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Perriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
COMMENT Rockville, MD 20850, USA
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VERSION BUI55617.1 GI:22669149
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AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NTH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCTD/DTF
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
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US-10-017-084A-523 (1-344) x BUI55617 (1-856)

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 VERSION CD354474.1 GI:31146975  
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 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC <http://mgi.nci.nih.gov/>  
 1 (bases 1 to 765)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgabbs-remail.nih.gov  
 Tissue Procurement: Dr. Jim Lin, University of Iowa  
 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
 Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
 This clone was contributed by the Brain Molecular Anatomy Project (BMAP)  
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 /clone\_lib="NIH BMAP GMO"  
 /note="Organ: Brain; Vector: pYX-Asc; Site 1: Ecor I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction. Ligated with Ecor I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTGAAT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

ORIGIN  
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 Pred. No.: 9.17e-19 Length: 765  
 Score: 1720.00 Matches: 247  
 Percent Similarity: 88.03% Conservative: 3  
 Best Local Similarity: 86.97% Mismatches: 3  
 Query Match: 71.43% Indels: 31  
 DB: 14 Gaps: 3

US-10-017-084A-523 (1-344) x CD354474 (1-765)

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Db 125 GTCAGGCAGGGGAGAGCGCCACCTCAGGTGTCACAAATTGACAAACCGAGTCACCGGGTG 184  
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 genomic survey sequence.  
 ACCESSION AY404090  
 VERSION AY404090.1 GI:39760073  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 11493)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,  
 Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.  
 Inferring nonneutral evolution from human-chimp-mouse orthologous  
 gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 11493)  
 Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,

Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
 Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
 Adams, M.D. and Cargill, M.

## TITLE

Direct Submission

## JOURNAL

Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
 Rockville, MD 20850, USA

## COMMENT

This sequence was made by sequencing genomic exons and ordering  
 them based on alignment.

## FEATURES

Location/Qualifiers

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## gene

## ORIGIN

## Alignment Scores:

Pred. No.: 3.02e-13 Length: 11493  
 Score: 1714.20 Matches: 303  
 Percent Similarity: 10.67% Conservative: 30  
 Best Local Similarity: 9.71% Mismatches: 8  
 Query Match: 71.19% Indels: 2779  
 DB: 29 Gaps: 243

US-10-017-084A-523 (1-344) x AY404090 (1-11493)

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QY      7 ----- 7
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QY 331 Pleu--Leu--Pro--Leu-----LeuVal----- 338  
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QY 338 uHisLeu----- 340  
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QY 341 -----LeuLeu-----Lys-----Phe 344  
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## RESULT 11

AK028345  
LOCUS  
DEFINITION Mus musculus 12 days embryo embryonic body below diaphragm region  
cDNA, RIKEN full-length enriched library, clone:3732419F12

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

product: weakly similar to OPIOID BINDING PROTEIN/CELL ADHESION  
MOLECULE PRECURSOR (OBCAM) (OPIOID-BINDING CELL ADHESION MOLECULE)  
(OPCML) [Homo sapiens], full insert sequence.  
AK028345  
GI:26390423  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus

## REFERENCE

Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636

## AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, K.,  
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Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes  
Genome Res. 10 (10), 1617-1630 (2000)  
20499374  
11042159

## TITLE

Shibata, K., Itoh, M., Aizawa, K., Nagao, K., Sasaki, N., Carninci, P.,  
Konno, H., Akiyama, J., Nishi, K., Kitsu, T., Tashiro, H., Itoh, M.,  
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,  
Yanamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,  
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,  
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
Okazaki, Y., Muranatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format  
sequencing pipeline with 384 multicapillary sequencer  
Genome Res. 10 (11), 1757-1771 (2000)  
20530913  
11076861

## JOURNAL

Medline  
PUBMED  
REFERENCE  
AUTHORS  
The RIKEN Genome Exploration Research Group Phase II Team and the  
FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)

## TITLE

The FANTOM Consortium and the RIKEN Genome Exploration Research  
Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation  
of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
6 (bases 1 to 2798)

## JOURNAL

Medline  
PUBMED  
REFERENCE  
AUTHORS  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P.,  
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,  
Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T.,  
Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T.,  
Katon, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,  
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,  
Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, I.,  
Sugabe, Y., Tagami, M., Tanaka, T., Tanaka, A., Takahashi, F., Takaku-Akai, S.,  
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
Muranatsu, M. and Hayashizaki, Y.  
Direct Submission

## TITLE

Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of  
Physical and Chemical Research (RIKEN), Laboratory for Genome  
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,  
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
Fax: 81-45-503-9216)

## JOURNAL

COMMENT  
cDNA library was prepared and sequenced in Mouse Genome  
Encyclopedia Project of Genome Exploration Research Group in Riken  
Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to

prepare mouse tissues.  
Please visit our web site for further details.  
URL:<http://genome.gsc.riken.go.jp/>  
URL:<http://fantom.gsc.riken.go.jp/>.

## FEATURES

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## ORIGIN

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US-10-017-084A-523 (1-344) x AK028345 (1-2798)

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18	Thr	GlyLeuAlaAlaLeu	Cys	24	206	202	SerAlaSer	Asp	206
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AUTHORS Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 11490)  
AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
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Db 2496 TCCAAACATAAATCATATCAGTAAACACATTAAGACAAATCCATCCTGGATCAAAAT 2555  
Qy 110 ----- 110  
Db 2556 TAATTTGAGTAAACACAGAAAGACTTAGAAAATTTCCCTAATCAGTTCAAAACCATTTAT 2615  
Qy 111 -----ProTyr----- 113  
Db 2616 AGATGTAATTTGGCTGTGAGTTACCTTTGACGTGTAGAAGACCTTACAGCTATAATGGAAC 2675  
Qy 114 -----Th 114  
Db 2676 CCTTTCCGACTGTCTTTAGAACTCAACAGGAAGCAAAAGTGAAGTGAAGTAGTAGTAC 2735  
Qy 114 rCyS-----Ser--Val----- 117  
Db 2736 GTGCTACAATACAGCAGATATTTATCTCTGTGGATGAATTTAGTCTCTGTGGACACAG 2795  
Qy 118 -----Gln----- 118  
Db 2796 GCTTATCATTTTCACTCAGAGTGAAGTCAATGTATTTGAAGTACTTGAAATGAGGA 2855  
Qy 119 -Thr-----Asp----- 120  
Db 2856 AACCAACCCAGTTTAGCACAAGATACAGTAATAATTAATAAATAATCCTGCTCTCCAA 2915  
Qy 120 ----- 120  
Db 2916 AGCATGAACACACCTGTCTTAAGTGTTTTAAAGAGGCTGCTAAGCTCAGAGACTTG 2975  
Qy 121 -----Asn----- 121  
Db 2976 CAGCAGCAGTAATAAAGCTTCCAGTAGTGAACCAAGTCATCTTGCAATCTTCAGAT 3035  
Qy 122 -----His----- 122  
Db 3036 CACAGTGAAGAATTCACCATGTGTTTCAAGAGATTGCTGATTTACAGTCGCCACTTTT 3095  
Qy 122 ----- 122  
Db 3096 TAGAGTCCAGATGATGACCCAGCTGCTCTCTTTGAAATGGCTAAGTCTGGCCATCAAA 3155  
Qy 123 -----Pro-----LysThr----- 125  
Db 3156 AAAGCCATCAGATGAGTTGTACAGAAACACAGTAGAGTGTACCAGTGGCTTCTGTGTAC 3215  
Qy 125 ----- 125  
Db 3216 TTGCATGGACACAGGAGGCTCTGAAGTTTTCCTCAGTGAGAGTGGAGAAGACTAGG 3275  
Qy 126 -----Ser----- 126  
Db 3276 ACTGGTTCCATGTGGGCGAGTAGGAGTTTCAAGTCTCAGAAATCCAGGACCAAGAGTGGAC 3335  
Qy 127 -----Arg----- 127  
Db 3336 AGTGAACACACATTTGAGAGGTTTGTCTATTTACCTTTACGAATAAAGACAGCTT 3395  
Qy 128 -----ValHisLeu----- 130  
Db 3396 GCCAGTTTCATATCAATGGGTCTTTGCTGTGTACATCAATAGGAAGAAATCTGGAAGAC 3455  
Qy 131 -----IleVal----- 132  
Db 3456 AGATACAAAGGAGATGGAATACCAGTTCATGAGACATGTTATTTGTGAAGACTTACTT 3515

Qy 133 -GlnVal-----Ser----- 135  
Db 3516 ACAGGTACTAGTGTCTTACGGGACCTGGCCACTAGTGGGAGCTAATGGATTATACTTA 3575  
Qy 136 -----Pro-----LysIleVal----- 139  
Db 3576 CTAATGAGTATGGCCGATCCTGATTTAGTTAGTATGATGATTTTCTGTAAATTTGCCAAGG 3635  
Qy 140 -----Glu-----Ile----- 141  
Db 3636 ATTTTATGAAGATATAGCTCATGAAAAAGGAAAGAACTGACCAAAAGTCTTCTCTGATGG 3695  
Qy 142 -Ser-----Ser-----Asp--Ile----- 145  
Db 3696 ATCTACTTGGGTTTCCATGAAGAACGTAAAGATTTCTAGATGACTCTATACTTTAAAGAAG 3755  
Qy 146 -----Ser-----Ile----- 147  
Db 3756 AGATGTTGGTTCAGCAGCCTTCAAGATATTTTGAATACCTCAAGAAGACTGGGTCCAA 3815  
Qy 148 -Asn-----Glu-----Gly-- 150  
Db 3816 AAACCTTTGTGCTGTGAACTTCTCTTCTGGTAAAAATTAGGATTTGAAGAAGCTGGCTG 3875  
Qy 151 -----Asn----- 151  
Db 3876 CAAACAGATACTACTTGA AAAACACATTTTCAGAGAAACAGTTTTTTCTGAAGTGTTTTT 3935  
Qy 152 -----AsnIle----- 153  
Db 3936 TCCAAATATTTCAAGAAATTTGAAGCAGAACTTAGAGATCCTTTAATGATCTTTGTTCTAAA 3995  
Qy 154 -----Ser-----Leu-----Thr--CysIle-----AlaTh 160  
Db 3996 TGAAGAAGTTGATGAGTTCTCGGGAGTTCTCGTGTACTCCATGATTTCTTGTTCCTT 4055  
Qy 160 r--Gly-----Arg-----ProGlu----- 164  
Db 4056 GGAGGGGCTCCTTTGGTTTGGCCATCAAGATGTCCACCCCGAAGGAGGAGTTCGAAA 4115  
Qy 165 -----Pro-----Thr----- 166  
Db 4116 GTTATTTGATTTAAAGATGGGAGATTCCTTATGTTTCTACTCAGGATTTATCTCAATCC 4175  
Qy 167 -----Val-----ThrTrp----- 169  
Db 4176 TATTAATTTGATTAATACTAGTTCAAGTTAGTATGGCAAAAGATGATTTTATGGGATGA 4235  
Qy 170 -----Arg-----His----- 171  
Db 4236 TATGCTAGAACGTCGACGTGTCAGTACGTGAAATTAATAAAGTGAATCATCTGCTGCATG 4295  
Qy 172 -----Ile-----Ser-----Pro-- 174  
Db 4296 CCTAAGAAGTAGTATCTTATGAGTCTTATCGATGAGAACTAAAAAATAAGGATCCTAG 4355  
Qy 175 -----Lys-----Ala-----Val----- 177  
Db 4356 AGCAAAAGGATTTTGGCTGCAAAATATCAAAACAATCCGCTTCTTCCATTTCTGCAAAAAC 4415  
Qy 178 -----GlyPhe--Val-----Ser-----Glu----- 182  
Db 4416 AGCAGGTTTCTTGGACTGGGAAGGCAACAGTTTAAAGCTGAAACCATGTTTGCAGC 4475  
Qy 183 -----AspGluTyrLeu--Glu-----Ile-----Gln----- 189  
Db 4476 AACTGACCTTTATACAGCTGAACATCAAGATATAGTTTGTCTTTTTCGAACCAATTTCTAAA 4535  
Qy 190 -----Gly-----IleThr-----ArgGlu----- 194  
Db 4536 TGAATAATCCCATCTTTTAGAGGTTGTGTTTCAGTGTCTATTTGGCTGTGTTAAAGAGTTTTT 4595

QY 195 -----Gln----- 195  
Db 4596 GGGATTACTCAAGAAGCCAAACAGTTGATCTGGTTATAAAACCAATTGAAAGAAGTAGCAA 4655  
QY 196 -Ser--GlyAsp-----Tyr--Glu-----Cys----- 201  
Db 4656 ATCAGTTGATGATGGAATTACACTGTACCAGAGAAATATCACCATGCTTGCTACAAATA 4715  
QY 202 -----SerAla----- 203  
Db 4716 CCTTCATGAAGCCTTGATGCAAAATGAAATCACTAAGATGTCATTAATTATGATAAGTTAAA 4775  
QY 204 -----Ser-----Asn-----Asp-----Val----- 207  
Db 4776 ACCCTTTAGCTTCATCTAGTTGAGAATGCATATGTGACTCGAAAAGGTTTCTTTTCA 4835  
QY 208 -----AlaAlaPro----- 210  
Db 4836 TTTAAATTTTGAGCGGCACCATACCTTTATCAGTTGCCTTAATAAGTATAAAATAATTT 4895  
QY 211 -----Val--ValArg----- 213  
Db 4896 CCGGAACTTTTGAACCGTGGGTGTGAGGCAGTCATGCACCTGTGAAGATTTTGCTCT 4955  
QY 214 -----Arg--ValLys--ValThr----- 218  
Db 4956 TGTTTGGAACTATTGATCAAGAAAGAGAAACAAATACAAAGAGAATTTTCA 5015  
QY 219 -----Val----- 219  
Db 5016 GCITTTGGCAGCAATATCAGTGAAGNATATGAGTCTCATTTAGAGAAAGAAACAAGA 5075  
QY 220 -----AsnTyr-----Pro----- 223  
Db 5076 ATTTTGTGAGAAAATTTATGCAAGATATTATGCCAGATACTAATCTTATGCTTCTCCC 5135  
QY 223 o-----Tyr-----Ile-----Ser----- 226  
Db 5136 TGCTAAATCGTTATGCTACAATGATGTCCTTGGATTAAGATTAAGGATACCACTGTAAA 5195  
QY 227 -----Glu-----Ala----- 228  
Db 5196 ATATTGTCATGCTGACATACCAGGAAGTAGCAGTAAACCTAGGAGCAGTCCCAAGCG 5255  
QY 229 -----Lys-----GlyThr----- 231  
Db 5256 ACACAAAGCCTTAGAAGATATGCATCCAATGCTGTTTAAACACACTTGGCAGCAATTT 5315  
QY 232 -Gly----- 232  
Db 5316 TGGCAGAAAGAAAATTTGACCAGCAGATTAAGAGCATCTTAATGCATATCCTTCTGA 5375  
QY 232 ----- 232  
Db 5376 AAAGGAATGTTGAAAGAGCTTCTTCAAAATGCTGATGATGCAAGGCGCAGCAATCTG 5435  
QY 233 -----Val-----ProVal----- 235  
Db 5436 TTTTGTGTTTGTATCCTAGACAGCATCCAGTTGATAGATATTTGATGATAAGTGGGCCCC 5495  
QY 235 ----- 235  
Db 5496 ATTGCAAGGCCAGCACTTTGTGTACAAACACAGCCATTTACAGAAGATGATGTAG 5555  
QY 236 -Gly--Gln-----LysGlyThr----- 240  
Db 5556 AGGAATTCAGATCTTGGAAAGAGGCAGAAAGAGGAAATCCTTATAAACTGGACAGTA 5615  
QY 240 ----- 240  
Db 5616 TGAATAGGATTCAAATCTGTGTATCATATCAGACTGCCATCTTTTATTTCTGGCAA 5675  
QY 240 ----- 240

Db 5676 TGACATCCTGTGTATTTTGTATCTCTCATGCCAGATATGACCAGGGGCCACATCCATTAG 5735  
QY 241 -----Leu-----Gln----- 242  
Db 5736 TCCCGAGCGCATGTTTAGAGATTTGGATGCGAGATTTTAGGACACAGTTCTCAGATGTTCT 5795  
QY 243 -----Cys----- 243  
Db 5796 GGATCTTTATCTGGGAACCCATTTAAACTGGATAATTTGCACAAATGTTCCAGATTTCTCT 5855  
QY 244 -----Glu--Ala-----SerAlaValPro----- 249  
Db 5856 TCGTAATGCAAGAAATGGCAAAAGTTTCGGAAATTTTCGTCTTCCAGCATTCAGACAGAAAT 5915  
QY 250 -----Ser-----AlaGlu----- 252  
Db 5916 GGTCCAGAAATCTTTTGGACAAACTGCGCTCAGATGGGCGCAGAACTTCTAATGTTCTTAA 5975  
QY 252 ----- 252  
Db 5976 TCACATGGAAATAATTTCTATTTTGCAATAGATAAGAGTACTGGAGCTCTAAATGTGCT 6035  
QY 253 -----Phe----- 253  
Db 6036 GTATTAGTAAGGGCAAAATCACAGATGGAGACAGATTGAAAAGGAACAATTTTCATGC 6095  
QY 254 -----Gln-- 254  
Db 6096 ATCTGTAATTGATAGTGTACTAAAAGAGCGCAGCTCAAAGACATACAGTTCAACAAT 6155  
QY 255 -----Trp----- 255  
Db 6156 AACCTATACTATGATCTAGGACTCTGAAGAAATCTTACTACGTGGCTAATTTGTAA 6215  
QY 255 ----- 255  
Db 6216 TAGATCAGGCTTTTCAAGTATGGAGAAAGTATCTAAAGTGTATATCAGCTCAAGAA 6275  
QY 256 -----TyrLys 257  
Db 6276 CCAAGATATTAATCTTTTCCACGTTGGGAGTAGTGCCTGCAATTAATCACAATATAA 6335  
QY 257 s----- 257  
Db 6336 AAAACCCCATAGGCGCTTCTGTTTTTGGCCTCTTTCTTTGGAGACTGGGCTGCCAATTCA 6395  
QY 258 -----AspAspLys-- 260  
Db 6396 TGTGAATGGCCACTTTTGCATCTGGATTTCAGCAGAGGAACCTGTGGCGTGATGATAATGG 6455  
QY 261 -----Arg-----LeuIle----- 263  
Db 6456 AGTTGGTCTTCGAAGTGACTGGAATAACAGTTTAAATGACAGCAATTAATAGCTCTGCA 6515  
QY 264 -----Glu-----GlyLysLys-----Gly----- 268  
Db 6516 TGTTGAAATGCTAATACAGTTTAAAAAAGCGGTATTTCCCTGGTCTGTGATCCACATATC 6575  
QY 269 -----ValLys----- 270  
Db 6576 AGTGTACAGAACACCCCTATTCATGTTGTAAGGACACTTTAAAGAGTTTTATCGTT 6635  
QY 271 -----ValGluAsnArg-----Pro----- 275  
Db 6636 TTTCCAGTT--AACCGTCTTGATCTACAGCCAGATTTATATTTCTAGTGAAGCACT 6692  
QY 276 -----PheLeu----- 277  
Db 6693 TTACAATTCATTCAGAAAGACATGAACGCTCTTTTACCTGTGTGGCGGCTCCAAATAT 6752  
QY 278 -----SerLysLeu-----Ile----- 281

Db 6753 TGATGGCTGACCTGCACTCTGCAGTTATAAATTAATCTTGATCAATATGTCTACTTTAA 6812  
QY 282 -----PhePhe-----AenVal-----SerGlu-----His----- 288  
Db 6813 TAAACTAGACCACTTTTGTGACAAATTTACTACAGGATGAAATCAACACACCTTAAATAATGC 6872  
QY 289 -AspTyr----- 290  
Db 6873 AGATTATAATATCAACACACGCAACAGTAGCAGAGAATGTCTATAGGCTGGAACATCT 6932  
QY 291 -----Gly-----Asn-----Tyr-----Thr----- 294  
Db 6933 CTTTTAGAAATGGTTTCAACTGGTTTATTAATCTGTGATGAACACTCTAATCTTTACCA 6992  
QY 295 -Cys-----Val-----Ala----- 297  
Db 6993 CTGCTTATAGATGACAGATATCTCTCTCTGACATAATGCAATATGGGAAGCTGCTTGTCTCT 7052  
QY 298 -----Ser----- 298  
Db 7053 TTTAATGACATTTCTCTCTCTGACATAATGCAATATGGGAAGCTGCTTGTCTCTCT 7112  
QY 299 -----Asn-----LysLeu----- 301  
Db 7113 GCACGACACTAATCTAAACTTTTTCATAGTTTAAACTTTTGTAGTTGATTGTTTAA 7172  
QY 302 -----Gly----- 302  
Db 7173 AGATGCAGAGAAATGAGATTGAAGTTGAGGATGTCCTCTCATCACACTGGACAG 7232  
QY 303 -----His----- 303  
Db 7233 TGTTTGCAAACTTTTGTATGCAAAAGCCAGCTTCTTAACAATATCAATGAAATTGAT 7292  
QY 304 -----Thr----- 304  
Db 7293 TCCATCCGCAAGACTTGTATTGATACATATATTTTGAATATAGTATATATTTTATT 7352  
QY 305 -Asn-----Ala-----SerI 308  
Db 7353 CAACCTGTAAGTTGCAAAAGTGTGACATTTCCAGCTTTGCTGATTTGTTCTCTGT 7412  
QY 308 eMet----- 309  
Db 7413 GTTGCTCGAATATAGACCAAAAGTTGCACAAAGTGGAAAGACATTTTGAAGTGA 7472  
QY 310 -----Leu----- 310  
Db 7473 GTCTTGGCTTAAGATGATGATGCTATTTTATTAGTGAATCTGTAAGTGTGAAGAAGATCA 7532  
QY 311 -----Phe-----Gly----- 312  
Db 7533 GGAAGAAACAAACCAACATTTGACATTTGATGATCTTAAAGACTGGGGCATTTGCT 7592  
QY 313 -ProGly-----AlaValSer-----Glu-----Val-- 319  
Db 7593 TCCAGAACAAAGTTTACTGTTTTCAGCCCAACAGCTTGTGGTCTCTGAAGGAGATTTCT 7652  
QY 320 -----Ser-----Asn----- 321  
Db 7653 GCTTCTCTCAGCCTTATGACATTTGACATTTGATGATCTTAAAGACTGGGGCATTTGCT 7712  
QY 322 -----Gly----- 322  
Db 7713 TCATGCTCTAATGAAGCTGGCTGTATTGCTTGTGTTGAACAAATCTGTTCCAAAGA 7772  
QY 322 ----- 322  
Db 7773 CAGTGCAATTTGTTCTTGTGTCATGTACACAGCAATATAGAGAGCCCCACACAGCAT 7832  
QY 323 -----ThrSer-----Arg----- 325  
Db 7833 CTTGAAGGCTCTACATTATATGTTCCAAACTTCAACATTTAGAGCAGAGAAAAATTAGTAGA 7892

QY 325 ----- 325  
Db 7893 AAATGATTTTGAGGCACCTTTTGATGATTTCAACTGATCAATTTGAATCAATTTGATGCCCA 7952  
QY 326 -----Arg----- 326  
Db 7953 AGATGATATAAAATTTCTAAAGTCACCTTCGGTCTATATAATCCATCAGTGGCGCTATGT 8012  
QY 327 -Ala-----Gly-----Cys-----Val 330  
Db 8013 AAGCATTTGAAAATTTTGAACATGCTACGTACTTACAAAAGTATCCCTTCAGCTGAAGT 8072  
QY 330 1-----Trp----- 331  
Db 8073 GGAGAAATGACACAATATCATCATCTGCTGCTTCTTGAAGAAAAATACACTTAAAGA 8132  
QY 332 -LeuLeu-----Pro-----Le 335  
Db 8133 ACTATATGAGGTGATTTGGTGTGCTGCTGATGATCTTTGAGGTATATTTGAAACACCT 8192  
QY 335 uLeu-----Val-----Leu-----HisLeu-----LeuLeu 343  
Db 8193 CTTACCAAAAATTTGAAAAATCTCTTTATGATGCAAAATTTAGACACTTGTATCTACTTAA 8252  
QY 343 a-----Phe 344  
Db 8253 GAATAGATATCAAGTGTCTGAGGAATATCAGAGATTAAGGAACAACCTTTT 8304

## RESULT 13

AK090134

LOCUS

DEFINITION

AK090134

8928 bp mRNA linear

Mus musculus 7 days embryo multipotent stem cell CRL-2070 NE cDNA,

RIKEN full-length enriched library, clone:G431003J08

product:meiotic check point regulator, full insert sequence.

AK090134

1 GI:26105747

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 Carninci, P. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374

11042159

3

Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,

Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M.,

Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,

Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,

Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,

Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsumura, S., Kawai, J.,

Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.

RIKEN integrated sequence analysis (RISA) system--384-format

sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

20530913

11076861

4

The RIKEN Genome Exploration Research Group Phase II Team and the

FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

TITLE





Db	1156	AGCACATCTCAGAAAGCCTCTCTCCAAAGCGGAATCCCTGTGGCTTCGCCGTTCAGAAATTA	1215
Qy	51	-----GluSer-----Ala-----Thr-----	54
Db	1216	CTCTTCATTACAGACCCAGAGTCGCTCAACCTCTTCGCCCCAGTCTACACTCTCGGTGCC	1275
Qy	55	-----LeuArgCys-----	57
Db	1276	TTCCATTTCCAAACATGGCGGCTCTAAGTCGTGCTCACTCTCTCGCTTAGTGTGCATC	1335
Qy	58	-----Thr-----	58
Db	1336	TTTCTCAGGGCGCAAGATTCAACCTTTCAAGCCACAGTCAGTCACCAAGAAGACACAG	1395
Qy	59	-----Ile-----AspAsnArg-----	62
Db	1396	CATTCTCACTCTCCGAGTGCAGTTTCAACGACTCATTTTGGCACACAGAAACAGAGCC	1455
Qy	63	-----Val-----Thr-----Arg-----	65
Db	1456	AATGTTCCTGAGCTGTGCATTGATGATCACTTATGAGCTGAGACACTTCGGAATATAGAGA	1515
Qy	65	-----	65
Db	1516	GAATAATTCTCAAGCTTCCAAGGTATTTATAACGACTGACTGTGTGGACAGAAAGTTCTT	1575
Qy	66	-----Val-----	66
Db	1576	GTGCTTTTGTGGAGGCCAGCTTCAGTTACGCTGTGTAAAGTTTCAAGAGAGTAATGA	1635
Qy	67	-----Ala-----TrpLeu-----Asn-----ArgSer-----	72
Db	1636	CAAGACTCAGCTTATCTTTGGCTCTGTCCACCAATACATACGAAAGACGACGCGCAGTG	1695
Qy	73	-----Thr-----IleLeuTyrAlaGly-----	78
Db	1696	GGGAAGATACACCATGCTGTCTTAGAAGGCAACGGGAACCTGGTGTACACAGGA	1755
Qy	78	-----	78
Db	1756	GTGTGCGGGTGGGAAGTCTTTATCCCTGGACTTCGGGCTCTTCCCTGCACAAATGTC	1815
Qy	79	Asn-----	79
Db	1816	AACATGATGCTCGGCCCGAGTACCCCGCTCGACGGTGTGTGTACTCCAAAGCCCTCAGT	1875
Qy	80	-----Asp-----	80
Db	1876	AAATTGCTTGGATCGATGGATGAGTGGTCTCTGTGTCTCAGTTCAGAAATTCAGGGAT	1935
Qy	81	-----Lys-----Trp-----Cys-----Leu-----	84
Db	1936	TCTTCAAAACCTTAATGATTCCTCTACAAATGAGGATTGCATTCAGCAGCTTGGAACT	1995
Qy	85	-----AspPro-----ArgValValLeu-----LeuSerAsn-----	93
Db	1996	TACATTCACTCTGTGGAGACCCCTGTTCAAAACAGAGTCACTCTAGAACCTGAGCAATGGC	2055
Qy	94	-----Thr-----GlnThr-----	96
Db	2056	TCCATGTTTCGATCACTATCCCTCAAGTGGCCACCTCGGAATTAGTACAAACGTGTCTG	2115
Qy	97	Gln-----TyrSerIle-----Glu-----IleGln-----	103
Db	2116	CAAGCAATTAAGTTTC--ATCTGCGAAAGAAGTAGCCATTTCAGGTGCTCGTCAAGTGG	2172
Qy	104	-----AsnVal-----	105
Db	2173	TACAAATGTGCAGTGTCCAGGAGGCCAGCTGTCACTCAGAGTGGAGTTTATTGTG	2232
Qy	106	-----ValTyr-----Asp-----	108

Db	2233	ATTGTGCTCTTGAACATGATGGGTTATACACAGACGGCTTAGCATGGACCGCAAGTTTT	2239
Qy	109	Asp---GluGly-----111	111
Db	2293	GACTTTGAAGGATCACTTTCCCGAGTCATTGCACCCAAAAAAGCAAGGCCTTCTGTGATACT	2352
Qy	111	-----111-----111	111
Db	2353	GGATCTGACGAGGACTGGGAGTACTTACAGAGTACCATCGCAATGTTGAGTCT	2412
Qy	111	-----111-----111	111
Db	2413	CATCTTTTGAACAAATCTCTATGTTGACTGCTTTGGAAGTTTCAAATGCAAGAGATGAA	2472
Qy	112	-----Pro---112	112
Db	2473	GATTTTTCGAGAACCTCAGCTCGGATTCCTTACCCCTCTCTTTGCTCACAATCCTGCA	2532
Qy	113	Tyr-----Thr-----114	114
Db	2533	ATTTCTTTGTTCTTACCTGGTTATGAAGAGTTCAAGTTGAATACTCTAATGGGAGAA	2592
Qy	115	CysSer-----ValGln-----ThrAsp---120	120
Db	2593	GGAATTTGTTCTCTTATCGACCTCTTGTTTCAGTTGGCAAGGACTTAAATTTGGACTCT	2652
Qy	121	AsnHis-----Pro-----LysThrSer---ArgVal---128	128
Db	2653	TACTTGGACCTACTACTACCGAGATTCGCCAACTCTTGTCAAAACCACTGCAGCAAGTATGC	2712
Qy	129	-----His-----129	129
Db	2713	ACCATTGACCAAGTCAGATGGGATTATATGATCATCCCCCAATTTTACTTCTGAGCCA	2772
Qy	129	-----129	129
Db	2773	CCAAGTATTATCAGTGGGTGAGTTCTATGCTGAAAGGTGAAGGGATGCGCGCTATCCT	2832
Qy	130	-----Leu---Ile-----131	131
Db	2833	TACCTTCTGGATTTCGAGAGAGCAGGCTAGTGGTCTTGTAGTATTCGCTCTATACC	2892
Qy	132	Val-----Gln-----Val---Ser135	135
Db	2893	CTTGGTGATGAGAGCTGTGTCTGTGTGTGATGAAACTTGCAGTACTTATCCAAAGTAAACCTCA	2952
Qy	136	Pro---Lys-----137	137
Db	2953	ACTCCCCAAAGGCCAAGCAGCAGCAAGAGAANAACAGTTTACTTTCGGCATTCGTCT	3012
Qy	138	Ile---Val-----Glu-----Ile-----Ser-----142	142
Db	3013	TCAGTTTCTGTTCTGGCCGAGAGATTAGTTGTCTGGATGGCCAGTGTAGGATTCACTTTA	3072
Qy	143	Ser-----Ser-----Asp---Ile-----145	145
Db	3073	AGAGATCTGGAGACTCTCCCTTTGGGATGTCTCTTCCCATCAGAGATTCGATTTACCAC	3132
Qy	146	-----Ser-----Ile-----147	147
Db	3133	TGTCGGGAGCAGCCTGATTACAGATTGGTTCAGAGCGGTCTGTCTTCTTGTATGGACGTCAG	3192
Qy	148	-----Asn-----148	148
Db	3193	GACCTTTTCAAGCAGGCTTGTGAAGGAATTTATCCAGAGGCAAAATCTGTGCTCTCATCA	3252
Qy	149	-----Glu-----Gly---Asn-----152	152
Db	3253	GAGGTGCTTCAGGAACCTGAGGCAGGAGGAGATGATGCCATGATGATGATGATGATGATGAT	3312
Qy	153	Ile-----153	153
Db	3313	GAGGTATGTCAATTAATGAGAGTGAAGATTATCGGGTGCAGGATGCGAAGGCTGCTT	3372

QY 154 ---Ser--- 156  
D5 3373 CAAGTGCACAGCCTGTCGCGTCAATGTGTGTCAGTACCCAGAACTCAGTACCAATGAG 3432  
QY 157 ---Cys--- 159  
D5 3433 TTCAATTGAAGAAAGAAACAGACTGCTCCAGTTGTGTGTCAGGAACTATGGCCCTTCCA 3492  
QY 160 ThrGlyArg 165  
D5 3493 GTAGGACGAGGAGTGTATTACCTTGTCTCATATCACCTGTTCCACAGAGCGGTGCT 3552  
QY 166 ---ThrVal--- 167  
D5 3553 GTTCTTAATTGATCTGACAGGGGAGCCCTCCACAGAAACAACTGTATGATCTTAAT 3612  
QY 168 ---ThrTrp--- 171  
D5 3613 AGCGAAACATCGACGTGCTCCCAACATGGCCAGCTGGGCCAGCTTTCATATGGTGTG 3672  
QY 172 ---Ile---Ser--- 173  
D5 3673 GTCGCGGCTGAAGATAGCCGAGCTCCAGATAGACTCAGCTTGGATCGTTTACAAC 3732  
QY 174 ---ProLys--- 179  
D5 3733 AAGCCAAAGCCTGCTGAGTTAGCAATGAGTATGCGCGCTTCTCATGCGCCCTGGTGTG 3792  
QY 179 --- 179  
D5 3793 AATGGCACCTTACCAAGCTGGCTACTCTCAATATCCATGACTATTGTACCAAGGCCAT 3852  
QY 180 ---ValSer--- 181  
D5 3853 GAATGACAAAGCATGGATTGTACTTGTGTGTTCTGCTGCAAGCTTGGCCACCATGGAC 3912  
QY 181 --- 181  
D5 3913 ATGTCAATTACCGGCTCCTCAGCATTCAGTTCTGCTCTCTTACCCCGCATCCACA 3972  
QY 182 Glu---Asp--- 183  
D5 3973 GAGCTGACGTGCTGCTCAATGTCCAAAGTGGGGCTGTGTTGGCATTTGGCCTTGTGTAT 4032  
QY 183 --- 183  
D5 4033 CAGGGCACAGCTCAGACACACTGCGGAAGTCTGTTGGCTGAATAGGGCGGCCCT 4092  
QY 184 ---GluTyrLeu--- 187  
D5 4093 GGTCCGAAATGGAATACTGCACTGACAGAGTCTACTCTCTAGCTGCTGGCCCTGGCC 4152  
QY 188 ---Ile--- 188  
D5 4153 CTGGGATGTTGCTTGGGGCATGSCAAATTTGATTGGCATGTCATCTCAATGTG 4212  
QY 189 ---Gln--- 192  
D5 4213 CTTGACAGCTGTATCAGTACATGTTGGAGGCCATAGGCGATTTCAAACCTGGAATGCAC 4272  
QY 193 ArgGlu--- 195  
D5 4273 AGGAGAAACATAAGTCTCAAGTTATCAGATCAAAAGAGGAGACACCATAAAGCTGGAT 4332  
QY 196 ---Ser---Gly--- 197  
D5 4333 GTGACTGTCCCGGTGCTACTCTGGGTTGGCTATGATCTACTTAAAAACCAATACAGG 4392  
QY 198 ---Asp---Tyr--- 199  
D5 4393 TCCATTGCTGATGGTGGTGTCTCTGATACCATGATTTGCTAGACTTTGTGAACCA 4452

QY 200 Glu--- 201  
D5 4453 GAATTCCTTTTCTTAGGACACTTGTCTGGTCTGATTTTGTGGATGATATCTTACCA 4512  
QY 202 ---Ser--- 205  
D5 4513 AATTCCAAAGTGGTTCAGGCAATGTTCTCAGATTATAAGAGAAATAGTATCTCTCTG 4572  
QY 206 ---Asp--- 206  
D5 4573 AGTGAATTTGAATTCCTTGTTCAGAGGACTTGAATTTGGAACCTTGTGCAAGCACAC 4632  
QY 207 Val--- 207  
D5 4633 GTCTACATTCATTCAGGAGCCTGTGCTCTAGGGTTTCGATTTGCTGGCTCAGAAAC 4692  
QY 208 ---Ala--- 209  
D5 4693 TTATCAGCATTTAGCTGTCTGCATAAATTTGCAAAAGATTTTATGAATTTATTTATCTGCA 4752  
QY 210 Pro---ValVal--- 212  
D5 4753 CCCAATGCTTCTGTAAACAGGGCCCTATAACCTCGAAACCTGCTGAGTGTGCTCTGCTG 4812  
QY 212 --- 212  
D5 4813 TCTCTGCCATGGTGTATGGCTGGCTCTGGAACTGGAAGTGTTCAGACTCTGTCTGCTTT 4872  
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D5 4873 CTGCACATGAAGACTGTGGTGGAGAGATGAATATGCTTCCACTTGGCCACCACCATGGCC 4932  
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D5 4933 CTGGCCCTTCTCTTTTGGAGGAGAAAGTACTCTTTTGGACATCCAACTCATCCATT 4992  
QY 212 --- 212  
D5 4993 GCTGCCCTTCTCTGTGCTTACCCACTTTCGCCAGCCACAGCACTGACAAACCGGTAT 5052  
QY 213 ---Arg---Vallys 216  
D5 5053 CATCTCCAGGCCCTTGGCACCTCTATGTGTAGCTGCGAAGCAAGGCTCTCTGTACT 5112  
QY 217 ValThrVal---Asn--- 220  
D5 5113 GTAGATGTGATACAAACACACACCCCTGTATGCCCTTATAGAAGTTACTTACAAGGCACT 5172  
QY 221 ---Tyr---Pro--- 222  
D5 5173 CAGTGGTATGAACAGACCAAGAGAACTGATGGCTCCAAACCTTCTTCCAGAACTTCTAT 5232  
QY 223 ---Pro---Tyr---Ile---Ser 226  
D5 5233 CTTTAAAGCAGATGAAGTTAAAGGGCAAGTACTGGGAACCTGCTCATGATTTAAGC 5292  
QY 227 ---Glu---Alalys--- 229  
D5 5293 AAGGAGAACAGCACTTGGGTCTATTTCTTCCAAAGATGGAGTTTATATGTAAGCTC 5352  
QY 230 ---Gly---Thr---Gly--- 232  
D5 5353 AGGGCAGCAGCTCTCTCTACAAAGAACCCCAATGGGGTGGCAGAGTTTGTGGCAACAA 5412  
QY 233 ---Val--- 233  
D5 5413 ACTGTGGCAATAGGAACCTGAGCCCGGCTTTCAAGCCCTGAAACAAATTCATCATTC 5472  
QY 234 ---Pro---Val--- 235  
D5 5473 ACTTCTGATCCAGCACTTCTGTCTATTGCTGAATATTTCTGCAAGCCGACTGTGAGCATG 5532  
QY 236 Gly--- 236

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Qy	236	-----	236
Db	5653	AAGAGAGACATGTCCAGACACATCTGATCTTTGGCAGATAAAGTTGATATTAGAAATTTTC	5712
Qy	237	-----	239
Db	5713	AGTTCCCGAAGCCACAGGATAGGCAGCATACCTATCCTAAGCTAGGGCTCTTCATAAAT	5772
Qy	240	-----	242
Db	5773	TCCGAGTTCTTACCTGTGGTGAAGTGCACTGTTGATGCTACCTCGTGGACCAAGTGGCTACAA	5832
Qy	243	-----	246
Db	5833	GCTGGCGGTGATGTGTGTGTCATCGCTCCTCACTAGTGGCAGCCTGTTGAGAAGTCTCAG	5892
Qy	247	-----	249
Db	5893	CTAAACATGCTGGCCTGCTCTCTTGTCTACACACTCTGTGCAGCAGCACACACTTGCC	5952
Qy	250	-----	253
Db	5953	CCCATGGGACTGGNAGGGAGCACAAAGCTTTGCTGACTCCTCTACAGGTTCCGGACACCTG	6012
Qy	254	-----	254
Db	6013	AAGATGCCGTCGGGCTTTGCTAAGACTGGCTCCTGTGCTTGGGAACCCACAGCCG	6072
Qy	254	-----	254
Db	6073	ATGGTCATGTGACCACTCTGCCGAGGGAACCCACCCTAGAAATGACTGTGGCACAGAA	6132
Qy	255	-----	255
Db	6133	TCCTGATGGCAGCAAGTGAAGGAGCATTTCTCTTTTGTAACTCAATGGAAGTCAAGTGC	6192
Qy	255	-----	255
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Qy	256	-----	258
Db	6253	CACGTGTCATGATGATATAAAACATCAGTTAAACTCACATTTGTGTAATTAAGATTTT	6312
Qy	259	-----	261
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Db	6493	TAACAGTTATCTTCTACAAATGATCTGTGCTTCCCGTGTGTGATGATGATGACACAGC	6552
Qy	266	-----	266
Db	6553	GTTACTGCCACAGTTTTTCTACTGATGAAGAATGTCTCAGATGGAGTACTGGACTGTG	6612
Qy	267	-----	271

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272	QY	-----Glu-----AsnArg--Pro-----	275
6673	Db	AAAGGCACTCTAAGGGGAGTCTATTTTGGTAGAATCGATGCTCTCTCAGAAGAGAAA	6732
276	QY	-----Phe-----	276
6733	Db	AAGAGATGATTTTCTCTCTGTACCATGTGAGAACTATAGCACAACTGCTCACAAACTAA	6792
277	QY	-----Leu-----	277
6793	Db	GAAGATTCCCTTGTGAGGACCAGTCACACAGCTTTGAGCTTTAGCACCTAGAAATATTA	6852
278	QY	Ser--LysLeu-----	280
6853	Db	AGCGATAAACTCCTGATGCTTGTCTGTGTGTACTTGGTGTGTCAGCCCTGTGCAGGCTGTG	6912
280	QY	-----	280
6913	Db	CATGACACCTGCTCAAAATFACTGAAATACAGAAATACCCCCACAGAGGAGTGTAAAGAA	6972
281	QY	Ile-----Phe-----	283
6973	Db	ATACGAAATCAGTCTATCTGAACCTAAAGGTCTGAAAGTGCTTTTGCACTTCGAGTTTC	7032
284	QY	-----Asn-----	284
7033	Db	AGGACAGCTCATGATGCCCATGTAAACAGAAACAACACTCCTTTCACCTCCATTTCAACCT	7092
285	QY	-----Val-----	285
7093	Db	GTGCTCACAGCTTCTCTCTCAGACCAAGTGTGACTGTAAACAAGTAGGAACTGCAGAAATGCC	7152
286	QY	-----Ser-----Glu-----	287
7153	Db	TACTCGTTAACTTCCCGCTGTGTTCTGAAAAAGCCAAATAGAAAATTGTCGTTGGGATTT	7212
288	QY	-----His-----AspTyr--	290
7213	Db	GGTAATGTCCATCTGCCTGCCTGCTCCCTGCAGCAGGTAATTTGTGGCTGACCTTGAG	7272
291	QY	-----Gly-----	291
7273	Db	GGCAAAATGTGCTTCTTCCTCACTTTTAGATTAGGAGATTGCAATTAATGGCAGTTGTGA	7332
292	QY	-----Asn-----Tyr--Thr--Cys-----ValAla--Ser--	298
7333	Db	TGAACATTCATTTGTATCAATATGAAACCACCTGTCCAAGTTATTTTTCCTCTCAATT	7392
299	QY	---AsnLysLeuGly--His-----Thr-----AsnAlaSerIle--	308
7393	Db	GTTAAT--GGCTGCCATGGAGGACTTGAAAGAGAGAGACTGAAT--TCAGTGAA	7443
309	QY	-----Met---LeuPhe-----	311
7444	Db	ACGCAATTGATGGCCCTTTTGTCCGCTGGACCGCACCAAGAAGAGATTCTTAGTGTCT	7503
311	QY	-----	311
7504	Db	TGAGTCAACCATGTTAGGATCTTCAGATAAATATTTACTAGTCTCCAACCATGCTGTG	7563
312	QY	Gly-----ProGly-----Ala	315
7564	Db	GGAAACCACTTACCATTGCACAGCAGCCACCTCTCTGGGAACCAACGCTCAAGGAGAGGCC	7623
316	QY	-----Val-----	316
7624	Db	CGAGAAACCTGAAGTGTCTTAGTATCAAAAGTGGCACTTGTGACTACAGGGAAGCCT	7683
317	QY	-----Ser-----Glu-----	318
7684	Db	GATTGCCAGCAGTGTGCTTCACTCTGTATCATGTGGATGGAGACACAAGGGGAGCT	7743



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 QY 41 -----AlaMetAsp-----43  
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 Db 1590 ATCCCAATTGAACCTCATGAACCCCGAGCCCTGGACTTCCACGCTGACAGCGGCTTC 1649  
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 QY 51 --GluSer-----Ala-----53  
 Db 1710 CGGGAGACCATCTGAAGGACGGCATCCACAATGTGGAGGGTGTGGCGTGGACTGGATG 1769  
 QY 54 -----Thr-----Leu 55  
 Db 1770 GGAGACAATCTGTACTGACGCGACGATGGGCCCCAAAAGACAATCAGCGTGGCCAGGCTG 1829  
 QY 56 -----Arg-----Cys-----Thr-----58  
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 QY 68 -----Trp-----68  
 Db 2070 CTCTACTGGGTGGATCGCTTCTACAGCGCATCGAGAGTACTGCTCAATGGCAGAC 2129  
 QY 69 -----LeuAsn-----70  
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 QY 71 -----ArgSer-----72  
 Db 2190 AACTACCTTCTTGACTGAGTATCGAGTGGCAGTGTCTACCGTGTGGAAGGGGTGTA 2249  
 QY 73 -----Thr-----Ile 74  
 Db 2250 GGAGCGCACCCCACTGTGACCTTCTGGCGAGTGGAGCGGCCCCCATCTTTGAGATC 2309  
 QY 75 --LeuTyr--Ala-----Gly-----Asn--79  
 Db 2310 CGAATGTATGATCCACAGCAGCAAGTGGCACCAAAATGCGGGGTGAACAATGGC 2369  
 QY 79 -----79  
 Db 2370 GGCCTGACGAGCTGTGCTTGGCCACCCTTGGGAGCCGCGAGTGGCGCTGTGCTGAGGAC 2429  
 QY 80 -----Asp-----80  
 Db 2430 CAGGTGTTGGAGCGCAGCGGCTCACTTGTGGCGAAACCCATCCTACGTGCTCCACCC 2489  
 QY 81 -----81  
 Db 2490 CAGTCCAGCCAGGCGAGTTTGCCTGTGCGCAACAGCCGCTGCATCCAGGAGCGCTGGAA 2549

QY 83 -----CysLeuAsp-----85  
 Db 2550 TGTGCGGAGACAACGATTGCTTGGGACAACAGTGTAGGCCCCAGCCCTCTGCCATCAG 2609  
 QY 86 -----Pro-----ArgVal-----Val-----89  
 Db 2610 CACACCTGCCCCCTCGGACCGATTCAAGTGGGAGAACACCGGTGCATCCCCAACCGCTGG 2669  
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QY 133 -----Gln----- 133  
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QY 134 ---Val-----Ser-----Pro---Lys-----Ile 138  
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QY 142 -----Ser----- 143  
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QY 149 -----Glu----- 149  
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QY 154 -----Serleu-----Thr-----Cys----- 157  
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QY 161 -----GlyArg----- 162  
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LOCUS AV318958 14278 bp mRNA linear HTC 15-JUL-2003  
DEFINITION Rattus norvegicus Aal064 mRNA, complete cds.  
ACCESSION AV318958  
VERSION AV318958.1 GI:32492561  
KEYWORDS HTC.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.  
1 (bases 1 to 14278)  
Xu, C.S., Li, W.O., Li, Y.C., Wang, G.P., Chai, L.Q., Yuan, J.Y.,  
Yang, K.J., Yan, H.M., Chang, C.F., Zhao, L.F., Ma, H., Wang, L.,  
Wang, S.F., Han, H.P., Shi, Q.B., Rahman, S., Wang, Q.N. and Zhang, J.B.  
Liver regeneration after PH  
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Wang, S.F., Han, H.P., Shi, Q.B., Rahman, S., Wang, Q.N. and Zhang, J.B.  
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University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.  
China  
FEATURES  
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VDRLOYMDIQGELERCISLVQSVTVVYISDMWTLAKNTIDFAEOYSTQKWAES  
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MUKNVKIPURFSPETILLNTFRVRSFTDLEIKAKIRITIDOMLSSELQWLPPEVY  
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QAAQFLNANPLVKSVPNSFNSKHVRMEHGKILVSGKALEGSDTVARLHTEKNT  
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GLKFLKTKTKQFDSLAKAQYKKNRDKSVPLKMPYEFMLNNSMDEKFEKVRDN  
VIPKARTPSVTIPGNNIIVPSVRLVPSLQLPVHIPTLTKFSPDPDKLSTIONI  
YIPAMGNFYDFSFSKSVITLNAGLYNQSLVARFLSSSFVTALQYKLGTSRL  
MRKVJUKATAVSLTNKFLKSHDSTISLTKKNMEASVKITANLHAPITFMNFKQELN  
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FLSQYSGSVANEANYLNSKGRSSRVLRQASNFAGIWNFVGENFAGEATLRIYIG  
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P."

ORIGIN  
Alignment Scores:  
Pred. No.: 3,06e-12 Length: 14278  
Score: 1684.30 Matches: 295  
Percent Similarity: 10.10% Conservative: 40  
Best Local Similarity: 8.89% Mismatches: 6  
Query Match: 69.95% Indels: 2977  
DB: 11 Gaps: 262  
US-10-017-084A-523 (1-344) x AY318958 (1-14278)  
Qy 1 Met-----LysThr---Ile-----Gln----- 5  
Dy 3718 CTGAGAGTTGAACCTCCAAAAGTGGGAGTCCGAGACTTCATATCCAGACACCTCTT 3777  
Qy 6 Prolys-----MetHis----- 9  
Dy 3778 CCTAAAACCTGATGGCGGAGTCAAATACACTAAACAGACAGACAGATGAGATTGACAT 3837  
Qy 9 ----- 9  
Dy 3838 TCCTTTGCTTTGGGTGGCAAGTCTTCAAAGAGCTCAAGAGTGCACAGAAAGTGTGAGGAC 3897  
Qy 9 ----- 9  
Dy 3898 ACCAGCCCTCAACTTCAAGTCTGTGGGGTTCCTCTCCGCTCTCAAGAGGTCCAGATTCC 3957

QY 10 -----Asn-----Ser----- 11  
Db 3958 CACTTTTCAATCCCAAGACACATCAGCTGCAAGTGCCCTCTCTTTGGGCAATTTCTGGAOCT 4017  
QY 12 -----IleSer-----Trp----- 14  
Db 4018 TTCCACAAATGCTACAGCAACTTGTACAACTGGTCTCAGTCTCTCTACACTGGTGGCAACAC 4077  
QY 14 ----- 14  
Db 4078 CAGCAGGATCACTTCAGCCTTCAGGCTCAGTACCGCATGAAGGCTGACTCTGTGGTTGA 4137  
QY 15 -----Ala-----Ile 16  
Db 4138 CCTGTTTTCCTACAGTGTCAAGGATCTGGAGAAACAACATACGACAGCAAGACACATT 4197  
QY 17 -----Phe-----Thr----- 18  
Db 4198 CACTTTATCGTGTGATGGGTCTCTACATCAATAATTTCTAGATTCCAAATTCAAAGTCAG 4257  
QY 18 ----- 18  
Db 4258 CCACGTGAAAAAATTTGAAACAACCCAGCTCTGAAAGGTTTATTACATTTGAAACATC 4317  
QY 19 -----Gly-----Leu-----AlaAlaLeu----- 23  
Db 4318 TAGTCCCTTGGGACCACAGATGCTGCTACAGTTACAGTTGAGCTGGAATCAAAAAAGAAACAAC 4377  
QY 24 -----Cys----- 24  
Db 4378 TCTGTATGTCAAAGACATCAAGGTTGACGAGATTCAGAGTATTTCATTGTACGCTCA 4437  
QY 25 -----Leu-----Phe----- 26  
Db 4438 AGTGAATATGSCCTGTCTTATGAGAGAGATTCTATGACTGGCCAGATGAGCGGAGAAATC 4497  
QY 27 -----Gln-----Gly-----ValPro 30  
Db 4498 CAACATGAAATTAATCCACCTACTTCCAGGACCAACACAGATAGTGGGAAATGTACCA 4557  
QY 31 -----Val-----Arg----- 32  
Db 4558 GGATGGAATGCTGTGTCTCACTTCCACCTCTGACCTGCAAGATGGCAVATTCAAGAACAC 4617  
QY 33 -----Ser----- 33  
Db 4618 AGCTTCCCTAAATATGAAACTATGAGTTGACTCTGAAATCCGACAGCAGTGGGCACTA 4677  
QY 34 -----Gly-----Asp----- 35  
Db 4678 TGAGAACTTTGCTGCTTCCAAACAGCTGGACATGACCTTCTTAACCAAGCGCACTGCT 4737  
QY 36 Ala-----Thr----- 37  
Db 4738 GCGTTCTGAACACAGGCCAACTACAAGTCCCTGAGACTTGTCAOCCCTTCTTCTGGATC 4797  
QY 38 -----PhePro-----Lys----- 40  
Db 4798 CCTCACTTCCAGGGGTAGAAATTAATCTGACATCTTTGGGACCGCAAAATTAATAC 4857  
QY 41 -----AlaMetAsp-----Asn----- 44  
Db 4858 TGGTGTCTCAAGTCAACGCTTAAGATTGCAACAGATGGAGTATCTACAGTGCACACCAC 4917  
QY 45 -----Val-----Thr-----Val-----ArgGln----- 49  
Db 4918 CAACTTAAAGTACAGCCGCTGCTGTGAGAAATGAGTTGAACGCGACAGCTTGGGCTCTC 4977  
QY 50 -----Gly----- 50  
Db 4978 TGGGGATCCATGAATTTGTCAACAGTGGCGCTTCAAAGAACACCATGTCAAAATTCAG 5037  
QY 51 -----GluSer-----AlaThr-----Leu----- 55

Db 5038 TCTTGATGGGAGAGCTGCCCTCACAGAGGTATCACTGGGAAGCATTTTACCAGGCCCATGAT 5097  
QY 56 -----Arg-----Cys-----Thr----- 58  
Db 5098 TCTGGGTGCAGACAGCAAAATGCTTCAACTTCAAACTCAGCCGAGAAGGACTGAAGCT 5157  
QY 59 Ile-----Asp-----Asn-----Arg----- 62  
Db 5158 ATCCAATGACATGATGGGCTCTCTAGCTGAAATGAAACTCGACCACACACACAGTCTGAG 5217  
QY 62 ----- 62  
Db 5218 AATTTCAAGTCTCTCCCTGGAGCTTCTCTCAAAAATGGAACAATATTATACAGTGGAGACAA 5277  
QY 63 Val-----Thr----- 64  
Db 5278 GTTTTATAAGCAGAATTTTAACTTACAGCTACAGCCCTATTCTTTTGGAAATTACTTTAAG 5337  
QY 65 -----Arg-----Val----- 66  
Db 5338 CAATGATCTGAAATATGATGCTCTAGTTTTCACCAACAATGGAAGTTTACGGCTGGAACC 5397  
QY 67 -----Ala-----Trp-----Leu-----Asn----- 70  
Db 5398 ACTGAAGCTGAATGGGTGGCAACTTTTAAGGGAACTTACCAAAATATGAGTGAACAA 5457  
QY 71 ----- 71  
Db 5458 CATCTATACCATCTCTTATAGTACCTGGTAGTAAAGTTTACAGAGCAGACACTGTAGC 5517  
QY 73 -----Thr-----Ile----- 74  
Db 5518 TACGTTTCAGGGTGTGGAGTTTCAGCCATAGCTAAATGCAGACATCGAAGGCTGGCTTC 5577  
QY 75 Leu-----Trp-----Ala----- 77  
Db 5578 CTCGGTTGATGCTCACTACCACTACAGTTTCAAGTCCACTGTCATTTTAAATGTTTCCG 5637  
QY 78 -----Gly-----Asn 79  
Db 5638 CTTTGTCTGCGACCGTTTACCTTTGGGCGTCGACACACATACAAAGTGTGTGATGGAATA 5697  
QY 79 ----- 79  
Db 5698 GTCCCTCTGGGAGAAACACACTGGGCGATGTA CAGTAAATTTCTGTTGAAAGCAGAAC 5757  
QY 79 ----- 79  
Db 5758 TCTGGCACTTACCTTCTCTCATGACTACAAAGGATCCACAGAGCCACATCTCCTGTACAA 5817  
QY 79 ----- 79  
Db 5818 GAACAGCTCAGTACAGCTCTTGAGCACA CACTCAGTGCCTTGTGCTACTCCAGCTGAACA 5877  
QY 80 AspLys----- 81  
Db 5878 GACAGCAGCTGGAAATTTCAAGACCGCCTGAATGACAAAGTATACAGCCAGGAATTTGA 5937  
QY 82 -----Trp 82  
Db 5938 AGCCTACAACACTAAAGACAAAATTTGGTATCGAGCTTAGTGGCGGCTGACCTCTCTGG 5997  
QY 83 -----Cys----- 83  
Db 5998 GCTGTACTCTCCAATTAAGTGGCGTTTTTCTACAGTGGCCTGTCAATGTCTTAAATAG 6057  
QY 84 Leu-----Asp-----ProArgVal----- 88  
Db 6058 CTTGGAGATAAATGATGCCCTTTGAGAGCCCCCGAAGATTCAAATGATGCTGTGGTGA 6117  
QY 89 -----ValLeu----- 90  
:::|

Db 6118 ATACGATAGAA CCAAGATGTCACACTATCAGCCTCCCATTTCTTCCAAAGCCTGCCAGA 6177  
Qy 91 Leu-----Ser-----Asn-----Thr-----111  
Db 6178 TTATTTGGAGAGAAATCGAAGAGGAAATTATAAGTCTACTGGAAGCCATGAAGGGGAATT 6237  
Qy 95-----Gln-----Thr-----Gln-----97  
Db 6238 ACAACGCTCAGTGTGATCAGTTTGTGAGAAATATAGATGGCCCTGAGCAGGCTTCC 6297  
Qy 98-----TyrSer-----Ile-----Glu-----101  
Db 6298 TCACAGATTTCATGATTCTGATGCTGCTGCTGAGAGACAGTAGCTGGTGCAA 6357  
Qy 102-----Ile-----102  
Db 6358 GGAAATTAATCTTTTCATGGAAACTATAGAAATACAGATAATGATGCTAATTGC 6417  
Qy 103-----GlnAsn-----104  
Db 6418 CTTAGATGAGCCAAATCAACTTGAATGAAAGAACTCTCTCAACTTGAGACATACGGAT 6477  
Qy 105-----Val-----105  
Db 6478 ACAATTTGATCAGTATATTAGAGATAATTATGATGCACAGACTTAAAGAACTATTGC 6537  
Qy 106-----Asp-----Val-----Tyr-----108  
Db 6538 TCAGATTATTGATAGAATCATTGAAAGCTTAAAGTCTTGAAGCAGTATCATATCCG 6597  
Qy 108-----108  
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Db 6718 AATCCAGATACAGAAAACTCCAGCATCTCAGAACACAGATTCAATAATAGACATCA 6777  
Qy 111-----111  
Db 6778 ACAGCTTGCTCAGAGTTAAACACACAGATTGAAGCTCTTGATGCCAATGCATTAGA 6837  
Qy 112-----Pro-----112  
Db 6838 TCAACTGAGAACTGCAATTTCTATTCCAAAGAAATAAGTGTCAATTATTGAGCGTGCAATA 6897  
Qy 112-----112  
Db 6898 CTTTGTATGAATCTTATTGAAGATTTTAAAGTAACCTGAGAAATCAATACTTTTAGAGT 6957  
Qy 113 Tyr-----113  
Db 6958 TATAGTCGTGAGTTAAATTGAGAAATATGAAGTAGACCGCAAAATCCAGGTTTAAATGGA 7017  
Qy 113-----113  
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Qy 114-----Thr-----114  
Db 7078 TGTGCTACGCAAAATTGAGATAAAGACTACTATGATAAAATTGGTTGTTTATTGATGA 7137  
Qy 115-----Cys-----SerVal-----Gln-----Thr-----119  
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Qy 120-----Asp-----120  
Db 7258 CAACAGCAAAATCCGTGAGATGACTCAGAGAATCAATGCTGAAATCCAAAGCTCTCGAACT 7317  
Qy 121-----AsnHis-----122  
Db 7318 CCACAGAAAACCTGAAGCAATTAAACTGTGGGTAGAGACTTCAAAACCCAGCTCTCCAA 7377  
Qy 123-----Pro-----LysThr-----Ser-----Arg-----127  
Db 7378 CTCCTCGTGAAGAACTCAAGGACACCAAGTAATACTGTGGTCTGTGATTGGCTGCAGGATGG 7437  
Qy 128-----Val-----128  
Db 7438 TTTGGCTCAATAAAGCCCAATTCAGATGCTTTAGAAGATGTACGAGACCGAATTTA 7497  
Qy 129-----His-----LeuIleVal-----Gln 133  
Db 7498 TCAATGGACATTCAGGGGAACTGGAGCGCTGCTGTCTCTGTTAAGCCAGTTTACAG 7557  
Qy 134-----Val-----Ser-----135  
Db 7558 CACAGTGGTCACTACATTTCTGACTGTGGACTCTGACTGCTTAAAAACATAACAGACTT 7617  
Qy 136-----ProLysIleVal-----Glu-----140  
Db 7618 TGCAGAGCAATATTCACCCCAAAA-----GTGGGTGAGAGTGTGAAAGCACTGTGTGAACA 7674  
Qy 141-----Ile-----Ser-----Asp-----Ile-----145  
Db 7675 AGGATTCAITGTTCTCTGAAATCCAAACATTTCTGGGGACCATGCTGCAATTTGAGTCTAG 7734  
Qy 145-----145  
Db 7735 TCTCCAGCTCTCCAAGAAGCTAACTTTCAGACTCTCTGACTTTATAGTCCCTTTGACAGA 7794  
Qy 146-----SerIleAsn-----148  
Db 7795 TTTGAGATTCCATCAATTTGGATAAATCTCAAAATGTTAAAGATGTTAAAAATCCCAATT 7854  
Qy 149 Glu-----149  
Db 7855 GAGATTTTCCACTCCAGAAATTCACCTCTCTCAACACCTTCCGTGTCCGTTCCTTTACAAT 7914  
Qy 150-----GlyAsn-----Asn-----152  
Db 7915 TGACTTGTGGAATAAAGCAAAAGATCATTCGAACTATCGACCAATGCTGAGCAGTGA 7974  
Qy 153-----Ile-----Ser 154  
Db 7975 GCTACAGTGGCCTTCCAGAGTGTATTGTGAGAGACCTGGAGATGTTGAACATTTCTCT 8034  
Qy 155-----LeuThr-----Cys-----Ile-----158  
Db 8035 TGCAAGACTCTCTCTGCAGACTTCCATGTACAGAAATCACAATTCAGAAATTCACAAT 8094  
Qy 159-----Ala-----ThrGly-----161  
Db 8095 CCCAAATGTCAAATCTCAAGATTTACAGGTTCTCTGATCTTCACATACAGAAATTCAGCT 8154  
Qy 162-----ArgProGlu 164  
Db 8155 TCCTCACCTCTCATGCAAACTGAAATACCTGTTTCGGCAAACTACATAGCGTCTCTGAA 8214  
Qy 165-----Pro-----165  
Db 8215 AATCCAATCTCCCTCTTTTATATTAGATGCTAGTGCCAAACATACAGAACTACTACTTC 8274  
Qy 165-----165  
Db 8275 AGAGAACAAAGCAGAGATTGTGGCTTCTGTCTGCTGCGCAGGAGAGTCCAAATTTGAGC 8334

QY 166 -----Thr-----Val----- 167  
Db 8335 TCTCAATTTTGATTTTCAAGCACAGCTCAGTTCCTGGAGTTAAATGCTAATCCTCTGGT 8394  
QY 168 -----Thr----- 168  
Db 8395 ACTGAAGGAATCGTGAACTTCTCCAGTAAACATGTGAGAATGGAGCATGAGGTAAGAT 8454  
QY 169 -----Trp-----ArgHis-----Ile----- 172  
Db 8455 ATTAGTTTCTGGAAAGCCCTTGAGGAAAATCAGACACGGTTGCAAGATTACACACAGA 8514  
QY 173 -----Lys-----AlaVal-----Pro 174  
Db 8515 GAAAAATACAGTGGAGTTTAATAGTATGTGTGTCAGATAAACAATCAATTCACCC 8574  
QY 175 -----Lys-----AlaVal----- 177  
Db 8575 TGACAGTCAAAACAAAGTACTTCCACAAGTTGAGTGTCCCAGGTGGACTTCTCCAGTAA 8634  
QY 178 GlyPheValSer-----GluAsp-----Glu-----Tyr----- 185  
Db 8635 GGCTTC---TCTCAACATGAATCAAGACACTATTAGAAGCTGGACATATGGCATGGAC 8691  
QY 186 -----LeuGlu----- 187  
Db 8692 TTCCTCAGGACAGGTCATGAACTGGGCTGTCCCACTTCTCAGATGAAGGCATACA 8751  
QY 188 -----IleGln-----Gly-----Ile----- 191  
Db 8752 TTCATCCAAAATTAGCTTCATTGTGATGCCCACTGCTCTCTTTGGATTGTCCAATA 8811  
QY 192 -----Thr----- 192  
Db 8812 CATAAATGGCAACACCTAAGGGTTGTCCAAAACCTGACTTCTGAATCTGGTTCCTCAA 8871  
QY 193 -----Arg----- 193  
Db 8872 CTATTCTAGTTTGAAGTTGAGTCAAAAGTTGAATCTCAGCAGCTGGGCTCCAGATTCT 8931  
QY 193 ----- 193  
Db 8932 AACTGCCGAGGTCGGGCACTGCTTGGGGATGCAAGGCAGAAATGACTGGTGAGCACAA 8991  
QY 194 GluGln-----Ser-----Gly----- 197  
Db 8992 TGCCAACTTAATGGAAAAGTTATTGGAACGTTGAAAAATTCCTTTCTTTTCGGCACA 9051  
QY 198 -----AspTyr----- 199  
Db 9052 ACCATTGTGAGATTACTGCATCCACAAATAATGAAGGAATTTGAAAGTTAGTTTTCACAT 9111  
QY 200 -----Glu----- 201  
Db 9112 AAAGTTGACTGGGAAAATAGACTTCTTAAATAACTATGCACTGTCTTGAGCCCCCATGC 9171  
QY 202 -----Ser----- 202  
Db 9172 CCAACAAAGCAAGCTGGCAATTGAGTACTAGATTCAATCAGTACAAATACAAATTT 9231  
QY 203 -----Ala-----SerAsn----- 205  
Db 9232 TTCGGCTATAACAATCAGCACACATCGAAGCCAGTATAGTAATGAATGGAGATGCCAA 9291  
QY 205 ----- 205  
Db 9292 CCTGTATTTCTTAAACATACCTTTAACAATTCCTGAAATTAATCTACCTTTACACAGGTT 9351  
QY 205 ----- 205  
Db 9352 CACAACTCCCTTACTGAAGGATTTCTCCATATGGAAGAAAACGGGCTTGAAGAAATTTT 9411  
QY 206 ---Asp-----Val----- 207

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QY 208 AlaAla-----Pro-----Val----- 212  
Db 9472 CAAGCATCTGTGTTTATCCTCTGAAATGTTTTATGAGTTTATGCTCAACAATGTCAA 9531  
QY 213 -----Arg-----ArgVal 215  
Db 9532 TTCTTGGGACAGAAAATTTGAGAAAAGTCAGAGCAATGCAATTACATTTCTTACCGCATC 9591  
QY 216 -----Lys-----Val----- 217  
Db 9592 CTATAATGAAACAAAATTAAGTTTGATAAGTACAAAACATGAAAATTCCTCAATCAGCC 9651  
QY 218 -----Thr-----Val----- 219  
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QY 219 ----- 219  
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QY 220 -----Asn----- 220  
Db 9772 CGTCACAATTCAGGTCCTTAACATCATTTGTGCTTCTACAGAGTTAGTGTGCGTCTCT 9831  
QY 221 -----TyrPro----- 222  
Db 9832 ACAGTTGCCAGTTTTCATATCCCTAGAGTCTCTATTCAAGTTTTCCTCCAGATTTCAA 9891  
QY 222 ----- 222  
Db 9892 GAATTAAGCACTATTGACAAATATTATATTCAGCAATGGGCAATTTCACTATGACTT 9951  
QY 222 ----- 222  
Db 9952 TTCTTTTAAATCAAGTGTCACTACACTGAATCAATGCTGGACTTTTATAACCAATCAGA 10011  
QY 223 -----Pro----- 223  
Db 10012 TCTCGTGTGCTGTTTTCTTTCTTCTTCTTCTTCTTGTACGGATGCCCTCGAGTACAACT 10071  
QY 224 -----TyrIle----- 225  
Db 10072 AGAGGTATCATCACGTCCTGATGGGAAAAGTATTGAAGTTAGCCACCGCTGTCTCTCT 10131  
QY 225 ----- 225  
Db 10132 AACTAAACAAATTTTAAAGGAAGTCATGACAGCACCATTAGCTTAACCAAGAAAACAT 10191  
QY 226 -----SerGlu----- 227  
Db 10192 GGAAGCTTCAGTGAAAACAACTGCCAACCTCCACGCTCCCATTTTTCACAATGAAGTTCAA 10251  
QY 227 ----- 227  
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QY 228 -----Ala----- 228  
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Db 10432 GGGTTCGTTCCCTTTCACAGSAATATTCAGGAAGTGTGCGCAATGAGGCGAATGTGTACT 10491  
QY 235 -----Val----- 235

Db 10492 GAATTTAAGGTTACTCGTCTTCAGTAAGTTTACAAGGAGCCTCTAATTTTGCTGGAT 10551  
Qy 235 -----  
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Qy 236 -----Gly-----Lys-----Gly----- 239  
Db 10612 CACATGGGAACAAATATGATAAACCAATTTACAGGTATTTACAGTACTTTTGACACAAAGG 10671  
Qy 240 -----Thr-----LeuGln----- 242  
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Qy 243 -----CysGlu----- 244  
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Qy 244 ----- 244  
Db 10792 CTTGAACTAGCACTAAGAACCAAGAGTCTAGCTGGGAAAAGTGGTCCAGGTGAATC 10851  
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Db 10852 ACAGGTTCTTCAGCACAATGCACACTTCTCCAATGACCAGAAGAGTACGCCTTGACAT 10911  
Qy 247 -----AlaVal----- 248  
Db 10912 TGCTGGATCCTTAGAAGGACAGCTGTGGGACCTTGAAAAATTTCTTTTACCGGCATTTGG 10971  
Qy 248 ----- 248  
Db 10972 CAAGAGCTTGAGGAACTCTTACAGATAGACGGAAGCGTCAGTATCTTCAAGCTTCGAC 11031  
Qy 249 -----Pro-----Ser----- 250  
Db 11032 TTCTTTCACTATACAAAACCCGAATGGCTATCTCTCTCACTCCCTGTGCAAGAACT 11091  
Qy 251 -----AlaGlu----- 252  
Db 11092 GACTGATGATTCATTAACAGGCTGAAACTAAATGACTTCAGTGAATCAAAATCTA 11151  
Qy 253 -----Phe-----Gln----- 254  
Db 11152 TAAAGAAATTAAGTACTTTCACCATTTGCCCTCAACCTAACATGCTGCCCAAGTAAATTT 11211  
Qy 255 -----Trp----- 255  
Db 11212 CCTGGGGTTGATCTGTTAAACAATACTCTAAACGAGAGGCTCTCTGTCCCTTACCTT 11271  
Qy 256 -----Tyr-----Lys----- 257  
Db 11272 TGAGACAACTATACCTGAAATTCATTAAGTGTGTCGCCAGTTTACCTTCCAAAGAGCTT 11331  
Qy 257 ----- 257  
Db 11332 TCCCGTTGGCAACACTGTCTTTGATCTGAATAGCTAACCAACCTAAATTCAGATTTGA 11391  
Qy 258 -----Asp-----AspLys----- 260  
Db 11392 TCTGCCTAGTATACCCCTGCCAGAGACCAATTGAGATCCCATCCCTTGTGATCTCTGT 11451  
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Qy 263 -----IleGlu----- 264  
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Qy 265 -----Gly-----Lys----- 266  
Db 11572 ATTCTGGATTCACATGCGATTCACCTTGCAGTTTCTGGAGTATGCTCTAAAAGTTGT 11631

Qy 267 -----Lys----- 267  
Db 11632 GGGAAACACACAGGATTTGAAAATGATAAGTTTCACTATAAAATCAAGGAACACTTCAACA 11691  
Qy 267 ----- 267  
Db 11692 CTGTGACTTCAATGTGAGTATTAACGAGAGTGTATATTGAAGGACTTTGGGACTTGA 11751  
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Db 11812 AGAAGACAGACAAAGTGTGTCTGCCTCAGCAGCCTCCCAAGCCATAGGCACTGTGAGTCT 11871  
Qy 270 -----Lys----- 270  
Db 11872 GGATGCAAGCACAGATGACCAGAGTGTGAGGCTGAATGTCTACTTCCGCCCTCAGTCCCC 11931  
Qy 271 -----ValGlu----- 272  
Db 11932 TCCAGATAATAAACTCAGCATATTTCAAATGAGTGGAGGGCAAGAGAGTCTGATGTGA 11991  
Qy 273 -----Asn-----Arg-----Pro----- 275  
Db 11992 AACATACATCAAAATTAATCTGGGAAGAGAGCAGCTTTTCAGATTGCTAGACTCCCTAAA 12051  
Qy 276 -----Phe-----Leu-----SerLysLeuIle----- 281  
Db 12052 AAGCAATGTGCCAAGGCTTCTGAGGCTGTTTATGATTATGTCAAGAA--GTACCACCT 12108  
Qy 282 -----PhePhe----- 283  
Db 12109 GGGACATGCTTCTTCAGAGCTAAGAAAAAGCTTTCAGAAATGATGCTGAACAGCCATAAG 12168  
Qy 283 ----- 283  
Db 12169 GATGTTGATGAGATGAACGTGATGCCAGAGGGTAACCGTGATACCTACCAGAGTCT 12228  
Qy 284 -----Asn----- 284  
Db 12229 ATATAAGAAGATGTTGGCTCAGGAGAGCCAGATATCCTCGAGAAACTCAAGAAAATGGT 12288  
Qy 285 Val-----SerGlu-----His-----Asp----- 289  
Db 12289 GTTAGGAGTCTAGTATTAATCTCAGAGTACCACATGCGCAGTCAATGGCTGATGGA 12348  
Qy 289 ----- 289  
Db 12349 CTCAGTCATTCATTTCCGTGAAGTTCAATAGAGTCCAGTTCACGAGGAATGCTGGAACATA 12408  
Qy 290 -----Tyr-----GlyAsn----- 292  
Db 12409 TACTGTGCAAGACTTTTACATATAGCCATGAGGGAACCAAGAAAGTACTCTCTCAGCT 12468  
Qy 293 -----Tyr-----Thr-----Cys-----ValalaSer 298  
Db 12469 GTTTAATGGGTTAGACACCTGTTTTCCTAIGTTCAAGACCAAGTAGAAGAAATCAAGAGT 12528  
Qy 299 Asn-----Lys----- 300  
Db 12529 AATCAATGACATAACATTTTAATGTCCCTTTTCCCAACACCTTTGTAACCTTAAAGAGTGT 12588  
Qy 301 -----Leu-----Gly-----His-----Thr----- 304  
Db 12589 CCTATTGATTTTTCAGGGAGGACTTAAACATTTTATCCAACTTTAGGCCAACAGGATATCAA 12648  
Qy 304 ----- 304  
Db 12649 TTTTACAACATACTAAGTGACTTTCAGAGCTTTTGAGAGAGCTTTTAGACATCATAGA 12708



MLKNVLIPLRFSTPEFTLLNFRVRSEFTIDLEIKAKIIRTIQDMLSELQWLPPEVY  
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 EIPAFGLHSLVILKQSLPILFDASANTQNIITSENKARIIVASVTARGESFEALNEDF  
 QAQOQFELNANPLVLAKESVNSKVRMEHEGKIIVSGKALEGSDTVARLHETKNT  
 VENNGLIVKINNOFTLDQSKYFPHKLSVPRLPDSSKASLNNEIKTLLLEAGHMAWTS  
 GTGSMWACPNFDEGHSSKISFIVDGPISAFSLGNNINGKHLRVQKLTSSGFLN  
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 GNTKSPVTSSSITELNDFNSKLSHAAGKGVDPKPSLSLTSYLSIESFTKNIKGS  
 FLSEYSGVANANVYNTKSGTSSVRVLRQASNPAGIWNFEVGENFAGETURRIYG  
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 RPTVVDYKEVLLTLPVTPRTQYLCSEFLCELTLVSYPYPAHLASAAALLRLAHGQTQ  
 P"

## ORIGIN

Alignment Scores:  
 Pred. No.: 3,06e-12 Length: 14278  
 Score: 1684.30 Matches: 295  
 Percent Similarity: 10.10% Conservative: 40  
 Best Local Similarity: 8.89% Mismatches: 6  
 Query Match: 69.95% Indels: 2977  
 DB: 11 Gaps: 262

US-10-017-084A-523 (1-344) x AY321317 (1-14278)

QY	1	Met	---	LysThr	---	Ile	---	Gln	---	5
Db	3718	CTCAGAGTTCAACCTCCCAAGAGTGGGATGGCCAGACTTCCATATCCACAGACACCTCTT	3777							
QY	6	ProLys	---	MetHis	---		---		---	9
Db	3778	CTTAATAAAGTGGCCGAGTCAATATACACTATAACAAAGAACAGAAATAGAGATTGACAT	3837							
QY	9	---	---	---	---	---	---	---	---	9
Db	3838	TCCTTTGCTTTGGGTGGCAAGTCTTCAAGAGACCTCAAGGTGCCAGAAAGTGTGAGGAC	3897							
QY	9	---	---	---	---	---	---	---	---	9
Db	3898	ACCAGCCCTCAACTTCAAGTCTGTGGGGTTCCATCTGCGGTCTCAAGAGTCCAGATTCC	3957							
QY	10	---	---	Asn	---	---	---	Ser	---	11
Db	3958	CACCTTTTCAATCCCCCAAGACACATCAGCTGCAAGTGCCTCTCTTTGGGCAATCTGACCT	4017							
QY	12	---	---	IleSer	---	---	---	Trp	---	14
Db	4018	TTCCCAAAATGTCTACAGCAACTTGTGAACCTGGTGCAGTCTCCTACATCGGTGGCAACAC	4077							

QY	14	---	---	---	---	---	---	---	---	14
Db	4078	CAGCAGGGATCACTTCCAGCCTTCAGGCTCAGTACCGCATGAAGGCTGACTCTCTGTGTGA	4137							
QY	15	---	---	Ala	---	---	---	---	---	Ile 16
Db	4138	CTGTGTTTCTCTACAGTGTCAAGGATCTGGAGAAACAACATACGACGACGAAGACACATT	4197							
QY	17	---	---	Thr	---	---	---	---	---	18
Db	4198	CACCTTATCGTGTGATGGGTCTCTACATCATATAATTTCTAGATTCATAAATCAAGTCAG	4257							
QY	18	---	---	---	---	---	---	---	---	18
Db	4258	CCACGTAGAAAAATTTGGAAACAACCCAGCTCTCGAAAGGTTTATTAACTTTGAAACATC	4317							
QY	19	---	---	Gly	---	---	---	Ala	Ala	23
Db	4318	TAGTGCTTGGGACCAACAGATGTCTGTACAGTTTCAGCTGGACTCAAAAAAGAAACAAC	4377							
QY	24	---	---	Cys	---	---	---	---	---	24
Db	4378	TCTGTATGTCAAAGACATCAAGGTTGACGGACAGTTCAGAGTATTTTCATTGTACGCTCA	4437							
QY	25	---	---	Leu	---	---	---	---	---	26
Db	4438	AGGTGAATATGCGTGTCTTATGAGAGAGATTCTATGCTGGCCAGATGAGCGGAGAATC	4497							
QY	27	---	---	---	---	---	---	Gln	---	ValPro 30
Db	4498	CAACATGAAATTTAACTCCACCTACTTCCAGGGCCACCAACAGATAGTGGGAATGTACCA	4557							
QY	31	---	---	Val	---	---	---	Arg	---	32
Db	4558	GGATGGAATGCTGTCTGTCTCACTTCCACCTCTGACCTGCAAGATGCATATTCAGAACAAC	4617							
QY	33	---	---	---	---	---	---	Ser	---	33
Db	4618	AGCTTCCCTTAAATATGAAACTATGAGTTGACTCTGAAATCCGACAGTGGGCGAGTA	4677							
QY	34	---	---	---	---	---	---	Gly	---	Asp
Db	4678	TGAGAACTTTGCTGTCTTCCAAACAGCTGACATGACCTTCTTAAGAAAGGCGACTGCT	4737							
QY	36	Ala	---	---	---	---	---	Thr	---	37
Db	4738	CGGTTCTGAACACACAGGCGCAACTACAGTCCCTGAGACTTGTCACTTCTTCTGGATC	4797							
QY	38	---	---	PhePro	---	---	---	Lys	---	40
Db	4798	CCTCACTTCCCGGTGTAGAAATTAATGCTGACATCTTGGGCGCCGACAAAATTAATAC	4857							
QY	41	---	---	AlaMetAsp	---	---	---	Asn	---	44
Db	4858	TGGTCTCACAAGTCAACGCTAAAGATTGCACAGATGGAGTATCTACCTAGTGCACCAAC	4917							
QY	45	---	---	Val	---	---	---	Thr	---	ArgGln
Db	4918	CAACTTAAAGTACAGCCCGCTGCTGCTGGAGATGAGTTGAACGCGAGACTTGGGCTCTC	4977							
QY	50	---	---	Gly	---	---	---	---	---	50
Db	4978	TGGGGCATCCATGAATTTGTCAACAGTGGCGGCTTCAAGAAACACCATGCAAAATTCAG	5037							
QY	51	---	---	GluSer	---	---	---	AlaThr	---	Leu
Db	5038	TCTTGATGGGAGAGTGGCTTCCACAGAGGTATCACTGGGAGCATTTACCAAGGCCATGAT	5097							
QY	56	---	---	Arg	---	---	---	Cys	---	Thr
Db	5098	TCTGGTGCAGACAGCAAAAATGTCTTCAACTTCAAACTCAGCCGAGAGGACTGAAGCT	5157							



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QY 59 Ile-----Asp-----Asn-----Arg----- 62
Db 5158 ATCCAATGACATGATGGGCTCTACGCTGAAATGAAACTCGACCACACACACAGTCTGAG 5217
QY 62
Db 5218 AATTTTCAGGTCTCTCCCTGACCTCTTCTCAAAAATGGACAATATTTACAGTGGAGACAA 5277
QY 63 Val-----Thr----- 64
Db 5278 GTTTTATAAGCAGAAATTTTAACTTACAGCTACAGCCCTATCTTTTGGAAATTAATCTTTAAG 5337
QY 65
Db 5338 CAATGATCGAAATATGATCTCTAGTTTGGACCAATGAGGTACGGCTGGAACC 5397
QY 67 ---Ala-----Trp-----Leu-----Asn----- 70
Db 5398 ACTGAAGCTGAATGTGGGTGGCAACTTTAAGGGAACCTACCAAAATAATGAGCTGAAACA 5457
QY 71 ---
Db 5458 CATCTATACATCTCTATTACTGACCTGTAGTACAGGTTACAGAGCAGACACTGTAGC 5517
QY 73 ---Thr-----Ile----- 74
Db 5518 TACGGTTCAGGGTGTGGAGTTCAGCCATAGGCTAAATGCAGACATCGAAGGCTGGCTTC 5577
QY 75 Leu-----Tyr-----Ala----- 77
Db 5578 CTCGGTGTAGTCACTACCAGCTACAGTTCAGATCCCACTGCATTTTAAACAATGTTTCCG 5637
QY 78 ---Gly----- 79
Db 5638 CTTTGTCTGGCACCGTTTACCTTGGCGTCGCACACACATACAAGTGGTGATGGGAAAT 5697
QY 79
Db 5698 GTCCCTCTGGGGAGAACACACTGGCAGAGTACAGTAAATTTCTGTGAAAGCAGAAC 5757
QY 79
Db 5758 TCTGGCACTTACCTTCTCATGACTACAAAGGATCCAGGCCACAATCTCCTGTACAA 5817
QY 79
Db 5818 GAACAGGTCAGTACAGCTCTTGAGCACACACTCAGTGCCTTCTGCTGACTCCAGCTGAACA 5877
QY 80 AspLys----- 81
Db 5878 GACAAGCAGCTGGAATTCAGAGCCAGCCTGAATGACAAAGTATACAGCCAGGAATTTGA 5937
QY 82 ---Trp 82
Db 5938 AGCCTACAACACTAAAGACAAAATTGGTATCGAGCTTAGTGGACGGGCTGACCTCTGG 5997
QY 83 ---Cys----- 83
Db 5998 GCTGTACTCTCCAATTAAAGTGGCGTTTTCACAGTGAGCCCTGTCAATGTTCTTAATAG 6057
QY 84 Leu-----Asp-----ProArgVal----- 88
Db 6058 CTTGGAGATAAATGATGCGCTTTGACGAGCCCGGAGAATTCACAATGATGCTGTGTGAA 6117
QY 89 ---ValLeu----- 90
Db 6118 ATACGATAAGAACCAAGATGTCACACTATACGCTTCCCAATCTTCCAAAGCCTGCCAGA 6177
QY 91 Leu-----Ser-----Asn-----Thr----- 94
Db 6178 TTATTGGAGAGAAATCGAAGAGGAATATTAAGTCTACTGGAGGCAATGAGGGGAAT 6237
QY 95 ---Gln-----Thr-----Gln----- 97
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Db 6238 ACAAGCCCTCAGTGTGTGATCAGTTTGTGAGAAATATAGAGTGGCCCTCAGCAGGCTTCC 6297
QY 98 ---TyrSer-----Ile-----Glu----- 101
Db 6298 TCAGCAGATTCATGATTAATCTGAATGCACTGCTGGGAGAGACAAAGTAGTGGTGCCAA 6357
QY 102 ---Ile----- 102
Db 6358 GGAAAAATTAACCTCTTTCATCGAAAACTATAGAATTACAGATAATGATGTACTAATTGC 6417
QY 103 ---GlnAsn----- 104
Db 6418 CTTAGATAGTGC AAAATCAACTTGAATGAAAACTCTCTCAACTTGAGACATACCGAT 6477
QY 105 ---Val----- 105
Db 6478 ACAATTTGATCAGTATATTAGAGATAATTATGATGCACAGGACTTAAAAAGAACTATTGC 6537
QY 106 ---Asp-----Val-----Tyr----- 108
Db 6538 TCAGATTATTGATAGAAATCAATTGAAAAAGCTAAAAATGTGTGACGACAGTATCATATCCG 6597
QY 108 --- 108
Db 6598 TGTAAATCTAGCAAAATCAATCCATAATCTCTATTATTATTGTGAAAAATGTTGATCTTAA 6657
QY 109 ---Asp-----GluGly----- 111
Db 6658 CCAAATCAGTAGTAGTGTGCGTCTTGGATCCAAAATGTGGATACCAAAATATCAAAATCAG 6717
QY 111 --- 111
Db 6718 AATCCAGATACAAGAAAAAACTCCAGATCTCAGAACACAGATTCAATAATATAGACATTCA 6777
QY 111 --- 111
Db 6778 ACAGCTTGTGTCAGAGTTAAACACACAGATTGAAGCTCTTGATGTCCCAATGCAATTAGA 6837
QY 112 ---Pro----- 112
Db 6838 TCAACTGAGAACTGCAATTTCTATTCCAAAGAAATAAGTGTCAATTATTGAGCGTGC AAAATA 6897
QY 112 --- 112
Db 6898 CTTTGTATTGAATCTTATTGAAAGATTTTAAAGTAAGTGAAGAAATCAATPACTTTTAGAGT 6957
QY 113 Tyr----- 113
Db 6958 TATAGTCCGTGAGTTAATTGAGAAATATGAAGTAGACCGACAAAATCCAGGTTTAAATGGA 7017
QY 113 --- 113
Db 7018 TAAATCAATPAGAGTTGGCCCAACAGATACAGCCTGAGTGAGCGCTCTTTCAGAAAACTAAGTAA 7077
QY 114 ---Thr----- 114
Db 7078 TGTGCTACAGCAAAATGAGATAAAAGACTACTATGATAAAATTTGGTTGTTTATTGATCA 7137
QY 115 ---Cys-----SerVal-----Gln-----Thr----- 119
Db 7138 CACTGTGAGTGGATTAAAGCAGTGTCTTTCAAAAAATATCAATTGAAGAACTGAATAGATT 7197
QY 119 --- 119
Db 7198 GATTGACATGTCGGTGA AAAAGTTGAAAAGCCTTTTGATTATCACCAGTTTGTAGACAAAAC 7257
QY 120 ---Asp----- 120
Db 7258 CAACAGCAAAATCCCGTGAGATGACTCAGAGAAATCAATGCTGAAATCCAAAGCTCTCGAAT 7317
QY 121 --- 121
Db 121 ---AsnHis----- 122
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QY 213 -----Arg-----ArgVal 215  
Db 9532 TTCTTGGGACAGAAATTTGAGAAAGTCAGAGCAATGCAATTACATTTCTTACCGCATC 9591  
QY 216 -----Lys-----Val----- 217  
Db 9592 CTATATGAACACAAAATTAAGTTTGATAGTACAAAACGAAATTCCTCAATCAGCC 9651  
QY 218 -----Thr-----Val----- 219  
Db 9652 TTCCAGGACCTTTCAAATCGTGGACACACTATCCCAAGTTCTCAATGAAGTGTCTCC 9711  
QY 219 ----- 219  
Db 9712 ATTGTGCTAGACACACTGGCTTCCAGCCATGTGATCCCGAAGAAATCGGCACCCCAAG 9771  
QY 220 -----Asn----- 220  
Db 9772 CGTCACAAATTCAGGTCTTAACATCATTTGCGCTTCATACAGGTAGTGTGCGGTCTCT 9831  
QY 221 -----TyrPro----- 222  
Db 9832 ACAGTTGCCAGTTTCCCATATCCCTAGGACTCTATTCAAAGTTTTCCTCCCAATTCAA 9891  
QY 222 ----- 222  
Db 9892 GAAATTAAGCACTATTGACAAATTTATATTCCAGCCATGGGCAATTTACCTATGACTT 9951  
QY 223 ----- 223  
Db 9952 TTCTTTTAAATCAAGTGTATCACAACACTGAATCAATGCTGGACTTTTATAACCAATCAGA 10011  
QY 224 -----Pro----- 224  
Db 10012 TCTCGTGTGCTGTTTTCTTCTTCTTCAATTTGTACGGATGCGCTCGAGTACAAACT 10071  
QY 225 -----TyrIle----- 225  
Db 10072 AGAGGTATCATCAGTCTGATGCGGAAAGAAAGTATTGAAGTTAGCACCGCTCTCTCT 10131  
QY 226 -----SerGlu----- 226  
Db 10132 AACTAACAAATTTTAAAGGGAAGTCATGACAGCACCATTAGCTTAACCAAGAAACAT 10191  
QY 227 ----- 227  
Db 10192 GGAAGCTTCAGTGAAACAACTGCCAACCTCCACGCTCCCATTTTCAATGAACCTTCAA 10251  
QY 228 -----Ala----- 228  
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QY 230 Gly-----ThrGly-----ValPro 234  
Db 10372 CAGCTTAGAAAGTCTCACTTCTTCTTCCATTGAGTCATTTCCACCAAGGAATATCAA 10431  
QY 231 ----- 231  
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Db 10492 GAAATCTAAGGTACTCGGTCTTCAGTAAGGTTTACAGAGGAGCTCTAAATTTTGTGGGAT 10551  
QY 233 ----- 233  
Db 10552 CTGGAACCTTTGAAGTAGAGAAATTTTGTGGAGAGAGTACTCTCCGACGCATCTATGG 10611  
QY 234 -----Gln-----Lys-----Gly----- 239

Db 10612 CACATGGGAACACATATGATTAACCATTTACAGGTATTCAGCTACTTTGACACAAAAGG 10671  
QY 240 -----Thr-----LeuGln----- 242  
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QY 244 ----- 244  
Db 10792 CCTGAAAGCTAGCACTAAGAACCCAGNAGTCAAGTGGAAAGTGAAGTCCAGGTGAATC 10851  
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Db 10852 ACAGGTTCTTCAGCACAATGACACACTTCTCAATGACCAAGAAGAAGTACGCTTGAAT 10911  
QY 247 -----AlaVal----- 248  
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QY 248 ----- 248  
Db 10972 CAAGAGCTTGGGAACTCTTACAGATAGAGGAAAGCGTCAGTATCTTCAAGCTTCGAC 11031  
QY 249 -----Pro-----Ser----- 250  
Db 11032 TTCTCTTCACTATACCAAAACCCGAATGGCTATCTCTCTCACTCCCTGTCGCAAGACT 11091  
QY 251 -----AlaGlu----- 252  
Db 11092 GACTGATAGATTCATTTATACAGGGCTGAACTAAATGATTCAGTGGATCAAAATCTA 11151  
QY 253 -----Phe-----Gln----- 254  
Db 11152 TAAGAAATTAAGTACTTTCACCATTTGCGCTCAACCTTAACAATGCTCCCAAGTAAAT 11211  
QY 255 -----Trp----- 255  
Db 11212 CCTGGGGTTGATCTGTAAACAACTACTTAACCCAGAGGGCTCTCTGTCCTACCTT 11271  
QY 256 -----Tyr-----Lys----- 257  
Db 11272 TGAGCAACTATACCTGAAATTCATTAATTAAGTGTGCTCCAGTTTACACTTCCAAAGAGCTT 11331  
QY 257 ----- 257  
Db 11332 TCCGCTGGCAACACTGTCTTTGATCTGAATAAGCTTAACCACTAAATGACAGATTTGA 11391  
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QY 261 -----Arg-----Leu 262  
Db 11452 ACCTGCTGGATTTTATTCGTTCTTTGGAGNACTGACTGCACAGTTGGGATGCGCTC 11511  
QY 263 -----IleGlu----- 264  
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QY 269 ----- 269

Db 11692 CTGTGACTTCAATGTGAAGTATACCAAGATGCTATATTGTAAGGACTTTGGGACTTGA 11751  
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QY 273 -----Asn-----Arg---Pro--- 275  
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QY 276 -----Phe-----Leu---SerLysLeulle--- 281  
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QY 283 ----- 283  
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QY 289 ----- 289  
Db 12349 CTCAGTCATTCATTTCTGAAGTTCAATAGAGTCCAGTTCCAGGGAATGCTGGAACATA 12408  
QY 290 -----Tyr-----GluAsn----- 292  
Db 12409 TACTGTGACGACACTTTACATATAGCCATGAGGGAACCAAGAAGTTACTCTCTCAGCT 12468  
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QY 301 -----Leu-----Gly-----His-----Thr----- 304  
Db 12589 CCTATTGATTTCAGGGAGGACTTAAACATTTTATCCAACTTAGGCCAACAGGATATCAA 12648  
QY 304 ----- 304  
Db 12649 TTTTACAACAATACTAAGTACTTTTCAGAGCTTTTGGAGAGACTTTTGAACATCATAGA 12708  
QY 304 ----- 304  
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QY 307 -----SerIleMet----- 309  
Db 12829 CTTCACTGAGTTCAATGACTTTTGTTCATCCATCATCTCAAGAGGGTCTCTATAAGCTACA 12888  
QY 310 -----Leu-----Phe----- 311  
Db 12889 GCAGGTCCATCAGTATATAGAGGCTTTCGTGGAAGAGTATTTTGTATCCGAGTGTGGTGG 12948  
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Db 12949 CTGGACAGTAAATATTATGAATAGAAAGAAAGATGTTGACCTTATCAAGACCTTTT 13008  
QY 313 ----- 313  
Db 13009 GGCTCCTCTGAGGATTTCTACTCTGAATACAGTGTGACAGCTGCTGATTTGTTGTTCCAA 13068  
QY 314 -----Gly---Ala-----ValSer----- 317  
Db 13069 AATGTCAACTCAGGTTGAGCAATTTGTGCCAGGATATCAGAGAGTATCTTAGCATGCT 13128  
QY 318 -----Glu----- 318  
Db 13129 TGCTGACATAAATGGAAGGGGAGGAAAGGTTGACAGAGCTTTCTATTGTGTAAAGGA 13188  
QY 319 -----Val-----SerAsn----- 321  
Db 13189 AAGAATAAAGAGTGTGCTCACTGGGTGGCAGAAATAACGTCTGATTAACCTCCGGCAGCT 13248  
QY 322 -----Gly----- 322  
Db 13249 CCATTCCAACTGCAGGATTTTTCAGACCAGCTCTCTGGCTACTATGAAAAATTCGTTGC 13308  
QY 323 -----Thr-----SerArg----- 325  
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QY 329 -----Cys 329  
Db 13429 GGATTTTGAAGCTGCTGGAAGTTGGGATCGCCTGCTCTACAATGAAGCTTGTCTGT 13488  
QY 330 Val-----Trp-----LeuLeu----- 333  
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QY 334 -----ProLeu---LeuValLeuHisLeu-----Leu 341  
Db 13549 CGAGAGATTGAATATGGTTTCAGACCCCTTTCATCTGCTCTCCATCTGCCACCATGCTT 13608  
QY 342 -----LeuLys-----Phe 344  
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## RESULT 17

BC038478

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

1 (bases 1 to 8259)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, F., Bhat, N.K.,

BC038478 8259 bp mRNA linear HTC 19-NOV-2003  
Mus musculus filamin, alpha, mRNA (cdna clone IMAGE:4222918),  
containing frame-shift errors.

BC038478

BC038478.1 GI:23620444

HTC

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 8259)

Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,

Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stappleton, M., Soares, M.B., Bonaldo, M.F., Casavant, I.L., Schetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carnanci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Heiton, E., Ketterman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Greenwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalish, D.E., Schnerf, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 8259)

Strausberg, R.

Direct Submission

Submitted (04-OCT-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: [cgaps-f@mail.nih.gov](mailto:cgaps-f@mail.nih.gov)

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIHSC), Gaithersburg, Maryland

Web site: <http://www.nisn.nih.gov/>

Contact: [nisc.mgc@nih.gov](mailto:nisc.mgc@nih.gov)

Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghghi, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.

## REMARK COMMENT

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 80 Row: j Column: 1

This clone has the following problem: frame shifted.

## FEATURES

## source

1..8259

Location/Qualifiers

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="FVB/N"

/db\_xref="taxon:10090"

/clone="IMAGE:422918"

/tissue\_type="Kidney, normal. 5 month old male mouse."

/clone\_lib="NCI CGAP\_Kid14"

/lab\_host="DH10B"

/note="Vector: pCMV-SPORT6"

## ORIGIN

Alignment Scores:

Pred. No.:	2.55e-13	Length:	8259
Score:	1683.60	Matches:	273
Percent Similarity:	13.36%	Conservative:	53
Best Local Similarity:	11.19%	Mismatches:	10
Query Match:	69.92%	Indels:	2104
DB:	11	Gaps:	238

US-10-017-084A-523 (1-344) x BC038478 (1-8259)

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QY	3	Thrile	---	Gln	---	5
989	ACCGTACTTCTCTGTCTGTGTATGTCCTGAAAGTGCAGGACTCATAGGTGACTGTGC	1048				
QY	6	---	Prolys	---	Met	---
1049	TCTTGTCTGGCCAAACATATTGCCAAAGAGCCCTTTGAGGTGTATGTGGACAAGTCA	1108				
QY	9	---	---	---	---	9
1109	GTGATGCCAGCAAAAGTGAAGTGCCTCCAGGGCCCTGGTCTGGAGCCCAATATTGCCA	1168				
QY	9	---	---	---	---	9
1169	ACAAGACTACTTACTTTGAGATCTTCACTGCAGGAGCTGGCATGGGTGAGGTGGAAGTTG	1228				
QY	10	---	---	Asn	---	11
1229	TCATCCAGGACCCCTACAGGACAGAAAGGCACAGTGGAACTCAGCTGGAGGCCAGGGTG	1288				
QY	12	---	---	Tip	---	16
1289	ACAGCACCTATCGCTGTAGCTATCAGCCACCATGGAGGGTGTCCATACAGTACATGTCA	1348				
QY	17	---	---	---	---	17
1349	CCTTCGCCGGTGTCCCATCCCTCGTAGCCCTACACTGTCTGTTGCCAAGCCTGTA	1408				
QY	18	Thr	---	Ala	---	23
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QY	24	---	---	---	---	24
1469	AAACAGCCGACTTCAAGGTGTACAAAGGGCGCTGGCAGTGGGGAGCTAAAGGTCACTG	1528				
QY	25	---	---	Leu	---	25
1529	TAAAGGTTCCAGGTGAGGAGCGTGTAAAGCAGAGGAGCTTAGGGGAGTGTGTATGSC	1588				
QY	26	Phe	---	---	---	27
1589	TTTGAATATTACCTACAAATCCCTGGCACATACACTGTCCATCATCTGGGGTGGCCAG	1648				
QY	28	---	ValPro	---	Val	31
1649	AACATTGGTCTGAAGTCCGTTTGAGGTGAAGGTAGGCACTGAGTGGCAATCAGAAAGTT	1708				
QY	32	Arg	---	---	---	33
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QY	34	---	AlaThr	---	Pro	41
1769	GAGGCCATTGGTGTATGATGGGACCTTTGGGTTTCTCTGTGGAAGGTCCATCAGACGA	1828				
QY	42	Met	---	---	---	43
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QY	44	---	Asn	---	Val	46
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QY	47	---	Valarg	---	Gln	49
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QY 55 ---LeuArg---57
D 2069 AAGCATGCTGGGAAGGCTCTCTTCGAGTTCAAGTTCCAGACAAATGAGGGCTGCTGTGTG 2128
QY 58 ---ThrIle---AspAsn---Arg---62
D 2129 GAAGCAGACTCAGGACAAATGGCAATGGTACTTACAGCTGTTCTTATGTGCCAGAAG 2188
QY 63 ---Val---Thr---ArgValalaTrp---Leu---Asn---70
D 2189 CCAGTGAAGCACACAGCCATGTTTCTTGGGGAGGTGTCCAGCATCCCCCAACAGCTCTTTC 2248
QY 71 Arg---Ser---72
D 2249 CGGTGATGTGGAGCTGGCAGCCATCCAAACAAAGTCAAGGTGTATGTTCCAGGAGTG 2308
QY 73 ---ThrIleLeu---Tyr---Ala 77
D 2309 GCCAAGACTGGGCTCAAGGCCCATGAACCTACTACTTTACTGTGGATTGTACTGAAGCT 2368
QY 78 Gly---78
D 2369 GGCCAGGAGATGTCAGCATTTGGTATCAAGTGTGCCCTGGAGTAGTGGGCCCCCACTGAG 2428
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QY 83 ---Cys---Leu---Asp---85
D 2489 CCCTGTGGGGTGGCAGCTATACCATCATGTCCTTTTGTGTGACCCAGGCCACCCACC 2548
QY 86 ---Pro---ArgVal---Val---89
D 2549 AGCCCATCAGAGTCAAAAGTGAGCCTTCTCATGATGCCAGAGGTGAAGGCTGAGGGT 2608
QY 90 ---Leu---Leu---Ser---Asn---93
D 2609 CCTGSCCTAAATCGCACTGGTGTGAACTTGGCAAAACCCACCTTTCACAGTCAATGCT 2668
QY 94 ---Thr---Gln---95
D 2669 AAAACTGCTGGAAAGCAAGCTGGATGTCCAATTTCTCAGGACTGGCTTAAGGAGATGCA 2728
QY 96 ---Thr---96
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D 2969 GGTCAAGGCAAAAGTAGCATCCAAAGATTGTAGTTCCTCAGGTGCAGCGGTACCTTCCAAG 3028
QY 104 ---Asn---104
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QY 109 ---109
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QY 114 ---ThrCysSer---ValGlnThr---Asp---121
D 3329 GGTACATGCTCTGTGTCTTATGTATCCACTGAGCCTGGGGACTTACAACATCAACATCCTT 3388
QY 122 ---His---Pro---123
D 3389 TTTGTGACACCCACATTCCTGGATCCCATTCAGGCCCATGTGGCTCTCTTTTGTAT 3448
QY 124 ---LysThr---Ser---Arg---127
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QY 127 ---127
D 3509 CAGTTCCAAGTGGACTGTTCAAGTGTGGCAGTGTGCTGAGTTGACGATTGAGATCTGCTCT 3568
QY 128 ---Val---His---129
D 3569 GAGCAGGACTGCCAGCTGAAGTATACATTTCAAGACCATGGTGTGATGSCACACACCATTT 3628
QY 130 ---Leu---Ile---131
D 3629 ACCTATATTCTCTCTGCTGCTGGGCTTACACTGTTTACCATCAAGTATGGGGCCAGCCT 3688
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D 3689 GTGCCCAACTTCCCAAGCAAGCTACAGTGGAACTGCTGTAGATACCTCAGTGTACAG 3748
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QY 149 ---GluGly---150
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QY 258 Asp-----Asp-----LysArgLeu-----Ile 263  
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QY 310 LeuPhe-----GlyPro 313  
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VERSION AY404420.1 GI:39760397  
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REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS 1 (bases 1 to 12304)  
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,  
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 12304)





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Qy 95 -----GlnThr-----GlnTyrSer-----
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Qy 102 -----
|||
Db 2790 TGGACCTGTGATCTGGATGATGACTGTGGGGACCGGTCCGATGATCAGCCTCATGGCCC 2849
Qy 103 -----Gln-----AsnVal 105
|||
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Qy 120 -----AspAsn-----
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QY 180 -----ValSer-----Glu----- 182  
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QY 183 -----Asp-----Glu 184  
DB 4824 TGGTCTGATGCGGACTCAAGCCATCAAAAGGCAATTATCAACGGCACTGGCGTGGAG 4883  
QY 184 ----- 184  
DB 4884 ACCGTTGTCTCTGCAGACTTGCCCAACGCCACGGGCTGGCTGTGGAATCTCCCGA 4943  
QY 185 -----Tyr----- 185  
DB 4944 AATCTGTTTGGACAAGTTTACACACCACCAAGAACAGACAGATTAACTGGTCCCGCTGGAC 5003  
QY 186 -----LeuGlu----- 187  
DB 5004 GGCCTCTTCAAGATGCGGTGTGTCAGGCGCTGGAGACGCCACCGCTGTGCTGCCAC 5063  
QY 188 -----Ile----- 188  
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QY 189 -----Gln-----Gly----- 190  
DB 5124 GGGACAACCACTCTGCTCTTCTAGTGGCCAGAGGGCCCTGTGGGTGGCCATTGAC 5183  
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DB 5184 TTCCCTGAGAGCAAACTCTACTGGATCAGCTCTGGGAACCAACAATCAACCGTTGCAAT 5243  
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QY 195 -----Gln---Ser-----Gly 197  
DB 5304 GCCCTGGCCATCATGGGGACAAAGTGTGTGGGCGAGATCAGGTGTACAGAGATGGGC 5363  
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DB 5364 ACGTGCAACAAAGCCGCTCTGGGTCGTGCTGGGTAACAGTACACACCTGTTGGTT 5423  
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DB 5424 ATGCACATGAAGTGTATGACGAGAGCATCCAGCTAGAGCATGAGGGCCACCAACCCCTGC 5483  
QY 201 -----CysSer----- 202  
DB 5484 AGTGTCAACACGAGACTGTTCACAGCTCTGCTGCCACATCAGAGAGCATCGCTCC 5543  
QY 203 -----Ala----- 203  
DB 5544 TGTATGTGTACAGCGGTTACAGCCTCCGAGCGGACAGCAGGCCCTGTGAGGGTGTGGC 5603  
QY 204 -----Ser-----AsnAsp 206  
DB 5604 TCTTTTCTCTGTACTCTGTATACATGAGGAAATTTCGGGGGATTCCTACTAGATCCCAATGAC 5663

QY 207 -----ValAlaAlaproVal----- 211  
DB 5664 AAGTCGGATGCCCTGGTC-----CCAGTGTCCGGAATTCCTCTGGCTGTGGATCGAC 5717  
QY 212 -----Val----- 212  
DB 5718 TTCCATGCCGAAATGACACTATTATTATTTGGTGTGATATGGGCTTAAGCACCATCAGCAG 5777  
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QY 224 -----Tyr---Ile-----Ser-----Glu----- 227  
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DB 6258 TACTGGATGACAGAACTCAAGCCAAATGGCTTCCATCAAGCGCGGTGCAAGACAAATGCT 6317  
QY 233 -----ValPro-----ValGly----- 236  
DB 6318 ACAGACTCGGTGCTCTGAGGACAGGCAATGGTGTTCAGCTTAAGACATCAAGGTCTTC 6377  
QY 237 -----GlnLysGlyThr----- 240  
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QY 241 -----Leu-----Gln-----Cys----- 243  
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QY 244 Glu-----AlaSer----- 246  
DB 6498 GAAGACGGGGCTCATCGGAGAGTACGCTGGCTACTGCTCTACTCAGAGCGGACCATC 6557  
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DB 6558 CTCGAAGACATCCACTGTGGGATGAGGTTAACTCAACGACCGGTGCGGCTTTGAA 6617  
QY 249 -----ProSerAlaGlu----- 252  
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QY 254 Gln----- 254



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QY 328 Y----- 328
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QY 328 ----- 328
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QY 340 -----Leu-----Leu----- 341
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QY 342 -----LeuLeu-----Phe 344
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ACCESSION AY318958
VERSION AY318958.1 GI:32492561
KEYWORDS HTC.
SOURCE Rattus norvegicus (Norway rat)

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## ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

## REFERENCE

AUTHORS

1 (bases 1 to 14278)

Xu, C. S., Li, W. Q., Li, Y. C., Wang, G. P., Chai, L. Q., Yuan, J. Y., Yang, K. J., Yan, H. M., Chang, C. F., Zhao, L. F., Ma, H., Wang, L., Wang, S. F., Han, H. P., Shi, J. B., Rahman, S., Wang, Q. N. and Zhang, J. B. Liver regeneration after PH

## TITLE

Unpublished

## JOURNAL

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Xu, C. S., Li, W. Q., Li, Y. C., Wang, G. P., Chai, L. Q., Yuan, J. Y., Yang, K. J., Yan, H. M., Chang, C. F., Zhao, L. F., Ma, H., Wang, L., Wang, S. F., Han, H. P., Shi, J. B., Rahman, S., Wang, Q. N. and Zhang, J. B. Direct Submission  
Submitted (09-JUN-2003) Henan Bioengineering Key Lab, Henan Normal University, No. 148 Jianshe Road, Xinxiang City, Henan 453002, P. R. China

## FEATURES

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QY      88  ---ValLeuLeuSerAen 93
Dbb      12367 CAGGAAATGAATGACTGAGTCCATCAGCCATGTGACTGCCATGTGTACTTCTGAGTAAT 12308
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QY      97  ---Gln----- 97
Dbb      12247 AGCCAAATCTTCTTATATAGACTCTGGTAGGTATCACGGGTACCGCTCTGGGCATTCAC 12188
QY      98  ---Tyr-----SerileGluile----- 102
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QY      112  ---Pro-----TyrThr----- 114
Dbb      11770 GTCCAGATGAGCCTCTCCCTCCAAAGTCCCAAGTCCCTCAAATATACCATTCTCGTTATA 11711
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QY      126  ---Ser-----ArgVal----- 128
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QY      129  ---His----- 129
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QY      144  ---AspileSer----- 146
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RESULT 20
AY321317/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
XU, C. S., LI, W. Q., LI, Y. C., ZHAO, L. F., MA, H., WANG, L., WANG, S. F.,
HAN, H. P., WANG, G. P., CHAI, L. Q., YUAN, J. Y., YANG, K. J., YAN, H. M.,
CHANG, C. F., SHI, J. B., RAHMAN, S., WANG, Q. N. and ZHANG, J. B.
Liver regeneration after PH
Unpublished
2 (bases 1 to 14278)
XU, C. S., LI, W. Q., LI, Y. C., ZHAO, L. F., MA, H., WANG, L., WANG, S. F.,
HAN, H. P., WANG, G. P., CHAI, L. Q., YUAN, J. Y., YANG, K. J., YAN, H. M.,
CHANG, C. F., SHI, J. B., RAHMAN, S., WANG, Q. N. and ZHANG, J. B.
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Submitted (11-JUN-2003) Henan Bioengineering Key Lab, Henan Normal
University, NO. 148 Jianshe Road, Xinxiang City, Henan 453002, P.R.
China
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## ORIGIN

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US-10-017-084A-523 (1-344) x AY321317 (1-14278)

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QY	14	-----	-----Tyr-----	----- 14	
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QY 116 ----- 116
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QY 117 -----ValGln-----Thr----- 119
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QY 120 -----Asp-----AsnHisPro----- 123
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QY 124 -----Lys----- 124
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QY 265 -----Gly----- 265  
Db 7453 TTTTATTGAGCAAAACCAATCTGCAGCAATCAACGACAAGACAGTACTTGTGTCTCT 7394  
QY 266 Lys-----LysGlyVal-----LysVal----- 271  
::: |||  
Db 7393 GAGTTTCCAGGAGTTGGAGACCGTGGTTTGAAGTCTTCTACCCACAGTTTAAAGC 7334  
QY 272 -----Glu----- 272  
Db 7333 TTTCAGTTTCTGTGGAGTTCGAGAGCTTGGATTCAGCATGATCTCTGAGTCATC 7274  
QY 272 ----- 272  
Db 7273 ACGGATTTGCTGTGGTTTGTCTAACAACCTGGTGATTAATCAAGGCTTTCAACTTTT 7214  
QY 273 -----Asn-----Arg----- 274  
Db 7213 CACCGACATGCAATCAATCTATTCAGTCTTCAATGATATTTTGAAGACACTGCTT 7154  
|||  
QY 275 -----Pro----- 275  
Db 7153 AATCCACTCGACAGTGTCTATCAATAAAACCAACCAATTTATCATAGTAGTCTTTTATCTC 7094  
QY 275 ----- 275  
Db 7093 AATTGCTGACACATTACTAGTTTCTGAAGAGCTCACTCAGCGCTGTATCTGTGGGC 7034  
QY 276 -----PheLeu----- 277  
Db 7033 CAACTCTATTGATTTATCAATTAACCTGGATTTCTGGTCTACTTCTATTTCTCAAT 6974  
QY 278 -----SerLys-----Leu-----IlePhe----- 282  
|||  
Db 6973 TAACTCAGGACTATAACTCTAAAGATTTGATTTTCTCAGTTACTTTAAATCTTTCAAT 6914  
QY 283 -----Phe-----Asn-----ValSer-----Glu----- 287  
|||  
Db 6913 AAGATTCATAACAAGTATTGACAGCTCAATTAATGACACTTATTTCTTTGGATAGAAAT 6854  
QY 288 -----His-----Asp----- 289  
|||  
Db 6853 TGCAGTTCTCAGTTGATCTAAATGCAATGGGACATCAAGAGCTTCAATCTGTGTTTAA 6794  
QY 289 ----- 289

Db 6793 CTCGCAAGCAAGCTGTTGAATGTCTATATTATGAATCTGTGTCTGAGATGCTGGAGTTT 6734  
Tyr-----Gly----- 291  
QY 290 ----- 291  
Db 6733 TTCTGTATCTGGATTTCTGATTTGATATTGTTATCCACATTTTGGATCCAGACGCCACC 6674  
|||  
QY 292 -----Asn----- 292  
Db 6673 ACTACTACTGATTTGTTAAGATCAACATTTTCAACAATAAATAGAGATTATGGATTGA 6614  
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QY 293 -----TyrThr----- 294  
Db 6613 TTTTGTAGATTTCACCGGATATGATCTGTTCTGTCAGCATTTTGTAGCTTTTCAATGAT 6554  
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QY 295 -----Cys-----ValAlaSerAsn 299  
|||  
Db 6553 TCTATCAATAATCTGAGCAATAGTCTTTTAAAGTCTGTCATCATATAAATTTCTCTAAT 6494  
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QY 300 -----LysLeu----- 301  
Db 6493 ATACTGATCAAAATGTATCGCGTATGTCCTCAAGTTGAGAGAGTTTTCATTCAGATTGAT 6434  
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QY 302 -----Gly-----His----- 303  
Db 6433 TTTGGCACTATCTAAGGCAATTAGTACATCATTTATCTGTAATCTATAGTTTTCATGAA 6374  
|||  
QY 304 -----Thr----- 304  
Db 6373 AGAAGTTAATTTTCTTGGCACCAGTACTTGTCTCTCCAGTCAGATGCAATTCAGATA 6314  
|||  
QY 305 -----Asn-----Ala-----SerIle-----MetLeu----- 310  
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Db 6313 ATCATGATCTCTGAGGAAGCTGCTCAGGGCCACTCTATATTTCCTCACAACTGATC 6254  
|||  
QY 311 -----PheGlyPro-----Gly----- 314  
|||  
Db 6253 AACACTGAGGGGTTGTAATTC-----CCCCTTCATGGCTTCCAGTAGACTTATAATTCCTCT 6197  
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QY 315 -----Ala----- 315  
Db 6196 TCGATTTCTCCAAATAATCTGGCAGGCTTTGGAAGAATGGGAGGCTGATAGTGTGAC 6137  
|||  
QY 316 -----Val-----Ser----- 317  
Db 6136 ATCTGGTCTTATCGTATTTCCACACAGATCAATTTGTGAATCTCGGGGCTCGTCAAA 6077  
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QY 317 ----- 317  
Db 6076 GGCATCATTTATCTCAAAGCTATTAAAGAACATTGACAGGCTCACTGTAGAAAAACGGCAC 6017  
|||  
QY 318 -----GluValSer-----Asn----- 321  
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Db 6016 TTTAATTGGAGAGTACAGCCAGAGAGTCTAGCCCGTCCACTAAGCTCGATACCAATTTT 5957  
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QY 321 ----- 321  
Db 5956 GTCTTTAGTGTGTAGGCTTCAAATTCCTGGCTGTATACTTTTGTCAATTCAGGCTGTCT 5897  
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QY 322 -----GlyThr----- 323  
Db 5896 GAAATTTCCAGCTGTGTCTGTTTACGTGGAGTCAAGCAAGGCACCTAGTGTGTGCTCAAG 5837  
|||  
QY 324 -----Ser----- 324  
Db 5836 AGCTGTACTGAGCTGTTCTTGTACAGGAGATTGTTGGCTCGTGGATCTTTGTAGTCATG 5777  
|||  
QY 325 Arg-----Arg----- 326  
|||  
Db 5776 AGAGAAGGTAAAGTGCACAGAGTTCTGCTTCAACAGAAATTTACTGTATACATCTGCCAGT 5717  
|||  
QY 327 -----Ala-----Gly----- 328  
|||  
Db 5716 GTGTTCTCCCAAGAGGGACATTTTCCCATCACCATTGTGTATGTGTGTCGACGCCCAAGGT 5657



VTQMSDLSQVTVHLMASPTENADHCLDPLITKTHLLSSLTQRHNSRTTEBELS  
 ARDGPAPHTHOLYLIVLURIISWTTNTRDIAFLGYDYKKAVALKRNLSLEALKGLKID  
 PQMSAKPKRGPISPAQYPPHVSTPFSFGPKDSSGGAYMLQKLIETDRFVFTTEE  
 ESGMSDQCGIAACQTDIDYNNRCLIELVNCQMVLRGAETGCVISAAKQLQCOQH  
 HPAMYGDTLQKTSWTLCLDGMQYPAITTESSPTQDQROLWLEKVNIEHERERSLDSV  
 QELMESSGAQVGMVTTTTDMQPAQAQOQVORIISRCNCRMYIISVSHDIDPELAT  
 QIKPPEVHENQEKEDLLKKQSGAVDTFTLHHELEISNPAQYAMILLIVNNLLHVE  
 PARKESKKQVRQLEISNPERORSIIHLQEAQRHQAQVTHLQKQMYISIMKSL  
 QDQSNRELLDLNQLQLOLNOEKANLQLESEELNLLRCFKQFOLQORANKWELRQQ  
 EDVSVRRETFYFAQARWLTTEEDQGLIAELQRFLYSKVNSDDTAELHLEIGFQ  
 TMNNLLPNAIYKVLPRSSQSGQRLALRFLSKVRPPVGGISVKEHEVENVPLTIQ  
 LSHRFFHMMGFFPGRNVDEDEVDEEDKSLVTTGIPVVKPROLIATDDAVPLGSG  
 KGVAOGLRFSRGVRSFKLPEHPVDDIDMKERAAMNNSFIYIKIPQVPLCVSKGE  
 KNSVDWGLNLVLPCLEVHNNTWLDPMAMVKRDSRKALVAQVIKEKRLKPAITGSE  
 VNGKLETKCDLNMQQOEBEERKLLILGLSVGDKNPKKSIFFGRK"

## ORIGIN

## Alignment Scores:

Pred. No.: 1,03e-12 Length: 10481  
 Score: 1676.80 Matches: 292  
 Percent Similarity: 10.71% Conservative: 44  
 Best Local Similarity: 9.31% Mismatches: 6  
 Query Match: 69.63% Indels: 2795  
 DB: 11 Gaps: 249

US-10-017-084A-523 (1-344) x AK090138 (1-10481)

QY	1	Met		Lys		Thr		Ile	4
Db	10355	ATGGCGAGCGCTTCTTAATGCCATCTCCCAAGTGAGCACAGACTGGGAAGTTTATC							10296
QY	5							Gln	5
Db	10295	CCCCAAACCAACACTCTTAGACAAACAGGCGTGGAGTGAGGCACAGAGATCAGACT							10236
QY	6	Pro						Met	8
Db	10235	CCTTCCTTAGCTTATTGGCACAAGGAGAGCAATTACATTAGAAATATATATATATG							10176
QY	8								8
Db	10175	TTTTATATATATATCTTTTATAAAATTTATCATATCTTGATCAAAACTATCCCCAAC							10116
QY	9								10
Db	10115	CTTTCTGTGCCCCGAAAGCAGGAGTACTAGGCTTGGACAAATCCCTGGGTCTCTGG							10056
QY	10								10
Db	10055	TTTTCTTGCCCTGTGGCCCTGGGTCTAATCCATGAGAGGGAACCCAGCGCTTTGTCCA							9996
QY	11								11
Db	9995	CCATGCCCTGCAGGAGCAGGCGCAGCTGTTGAACAATGTCTCAGTTCCCATATGCCCCA							9936
QY	12	Ile							16
Db	9935	CAAACTCTGAGATGAAGGAGGCTCTGCCACCTCAAGTCCCTGG--ATCCTGAGC							9879
QY	17	Phe							18
Db	9878	CAGAGTCAATTTCTATCTGTAGTCACTTGGGTCTCCACATCACTTGGCCTGCCGAAGAT							9819
QY	19	Gly							22
Db	9818	GGACTCTTGCAGGGTCTTGTGCGCCACACTTAAACCAATGAGGAGCGAGCTTTCTC							9759
QY	23								25
Db	9758	TTCTTCTGCTGTGATGTTTCAGTCACTTTGTTTCTAGCTTTCCCGGACCTCAGA							9699
QY	26								28

Db	9598	CCCCGTGCAGGTTTCAGCCTTAGCTTTTCTTTGATTACCTGGGCAACGAGAGCTTTTCG	9639
QY	29	---ValPro	30
Db	9638	GCTGTCCCTTTTGACAGCCATGCGAAAGTCAGCCATGTCCACGCTGTGTGTGTGCTACTC	9579
QY	31	---Val-Arg	32
Db	9578	CAGACAGGTTAGCACCAAGTTAAGGTGCGCCCACTCCACACTGTCTTCTCACCCCTATA	9519
QY	32	---	32
Db	9518	ACTGACACACAGTGGAACTTGTGGGATTTTATATATATGAAGGAGTGTTCATGGCAGC	9459
QY	33	---SerGly	35
Db	9458	TCGCTCTTTTCATCTTTGTCAATATCATCAACTGGGTGCTCAGGTAATTTTGGAAATGATCT	9399
QY	36	---AlaThr--PheProLys	40
Db	9398	TCTGACTCCAGAACTCCTGTGTCAAGCCCTGTGCACGCCCTTCCGGAGGCCAGTGGTAC	9339
QY	41	---Ala	41
Db	9338	TGCATCATCTGTGTGATATCAGCTGCGGAGGCTTTACAACTGGTATTCAGTAGTCACCAG	9279
QY	42	-MetAsp	43
Db	9278	TTTGACTTATCTCTTTCATCACCACCTTCATCATCTTCTATCATTTTCAGCAGGAAGAA	9219
QY	44	---Asn--Val--Thr	46
Db	9218	AAAGCCCATCATCTTCTATGGAAGAACCGGTGGGACAGCTGGATGTGAGAGCACCACATT	9159
QY	47	---Val	47
Db	9158	TACCTCAAAGTGTTCCTTAACAGAGATACACCACAGGTGGCGGACTTTGTGGAAGAG	9099
QY	48	-Arg	55
Db	9098	GCGGAGGCTAGCTGTCTCCAGACTGGCAGGAACTCTGGGGCCTTAGAACCACTTATA	9039
QY	56	---Gln	58
Db	9038	AATAGCATGAGGAGAGGTTGTTCAAGTGAACCCAGCCCACTCCAGGAGATGTCTGCG	8979
QY	59	-Ile--Asp	61
Db	8978	TGTGTCAATCAGATTTATTACCTTGTGTAAAGGAACCTCTGTAGTCTCAGCTCAGCGAT	8919
QY	62	---Arg	63
Db	8918	GCCAGCTGTCCATCTTCTGTGAGCGGCAAGTGCCTGAGCAAGTAAGTAACCTCGT	8859
QY	63	1	67
Db	8858	GCGAGGACCACACTCACATCTCTCTGTGTGTTTTCGAAGCTCCATTTTATGCTCGCTG	8799
QY	68	---Trp	68
Db	8798	CAGTTGGAAATCCTTAAACATCTGATGAGGATGTTTCAGTTCTTCGCTTTCCAGCTGCG	8739
QY	69	-Leu	73
Db	8738	GTTCGCTTTTCTTGGTTCAGCTGTAAGTGTGTTTGGTTCAGTCCAG--CAAGTCT	8680
QY	74	---IleLeu	75
Db	8679	CATTCTTCTGTCTCCTCTGTAAGACTTCATGATAGATACATCTGCTTCCCTAGTGCC	8620
QY	76	---TyrAla	77
Db	8619	TTATCTGGGCCACATGCTGCGGCACAGGCTCTCTGAGGTGATGATGCTGCTGCGCTGCT	8560



Qy	77	-----	77
Db	8559	CCTCAGGATTGCTAGAGATCTCCAGCTGGAACCTCACGCGCTGTTCTCTTTTCACTATGCT	8500
Qy	77	-----	77
Db	8499	CCTTCCGCTTGGGGTCTCAGCTGGAGAAGCAGGTTGTGTGACAATGTCCAGAAATCATAGCAT	8440
Qy	78	-----Gly---Asn-----Asp-----Lys-----	81
Db	8439	ACTCAGCTGGGTGGTAGAAATTTCCAAATTCGTGGTGGATGAGAGTAAAGTATCCACAG	8380
Qy	82	-----	82
Db	8379	CCGCTTCTGCTTTTAAAGAGATCCCTCTTTTCCGTGTTCTCATGAACCTCAGGTGGCT	8320
Qy	83	-----Cys-----	83
Db	8319	TAATCTCAGTTGCTAGCTCAGGATCAATGTCATGGCTGTAGTAAATATAGTACATCCGGC	8260
Qy	84	-----LeuAsp-----	85
Db	8259	AATTACAACTGAAATGATCCTCTGGACTTGTCTGGGCTTGGCTTCCGCTGGCTGGT	8200
Qy	86	-----Pro-----	86
Db	8199	TCCAGTCTGTGTTGTGTTAACCATGCTCCCACTGCCTGCCACTTTCCATCAGCTCCT	8140
Qy	87	-----ArgVal-----ValLeuLeu-----	91
Db	8139	GAACAGAGTCCAGACTAGTTCCCGGTGCTCTCAATATTCTTCACCTTAACACAGAGCT	8080
Qy	91	-----	91
Db	8079	GTCCGCCATCCTGTTTCAGTAGGGCTGTTTCAGTGGTGGCAAAATCTGCATGCCATCTA	8020
Qy	92	-----Ser-----	92
Db	8019	ACAGGCAAGTCAGGAAGTCTTTTGTGTTTCAGTGTGTCAACATACCAAGCTGGATGGTGT	7960
Qy	93	-----Asn-----	93
Db	7959	GGCACTGCAGAACTGAGCTTTGGCAGCGATCAATGACACAGCCTTCTGTCTGCTC	7900
Qy	94	-----Thr-----Gln-----	95
Db	7899	CACGAGAACCATCTGGCAGTTAACCACTCAATAAGGCAGTTTCGGTGTATATGTCAT	7840
Qy	96	-----ThrGln-----	97
Db	7839	CTGTCTGGCAGGAGCAATGCCACACAATTTGGTCACTCATACCGGATTCCTCTCTGTGA	7780
Qy	98	-----Tyr-----	98
Db	7779	ATACTACAATCTGTCTGTCTCTTCAATCAGCTTCTGCCAATGTAAAGCACCTCTGTGATG	7720
Qy	99	-----Ile-----Glu-----	101
Db	7719	ATCCCTTATCAGCCGTCCTCACTGAAGCTGGAGTGTGACATGATGGTGGGACTTGGGCAC	7660
Qy	102	-----	102
Db	7659	TAGTGGGATACCCGGCTTTTGGCTTTTGGCTGACATCTGAGGATCAATCTTCAAACCTT	7600
Qy	103	-----Gln-----	103
Db	7599	TCAGGGCCTCAGTAGAGAGATTACGTTTGTAGTACAGCTGCTTTTTTGTAGCCATCATATA	7540
Qy	104	-----AsnVal-----	105
Db	7539	AGCCAAAGGCATGTGCCCTATTGTTGGTGTGTCCAGGAAATCCGTAATCTACCAAAATACA	7480

Qy	105	-----	105
Db	7479	GCTGGTGTATGAAAGGCAGGATCACCATCTCGAGCAGAAAGCTCCTCTTCAGTGGTGC	7420
Qy	106	-----	106
Db	7419	GATTGCTGTCCTGGTAAAGTAAAGGAAGACAGGCTCAATAGGTGGGCTTTTGTGATCA	7360
Qy	106	-----	106
Db	7359	AGGGATCAAGGCAGTGGTCAGCGTTCTCTTCAGTGGGTGAAGCCATCAGATGAACAGTCA	7300
Qy	107	-----	107
Db	7299	CCTGACTTAAGTCACTCACCATCTGGGTTACACTCCACTCAGAAATAAGGCGCGCATCA	7240
Qy	108	-----	108
Db	7239	CTGTGCAGCTTGAGGTATAAGCGGTGAGTTCCTCCGAGTGAAGACATGGCCCTGACTGC	7180
Qy	109	-----	113
Db	7179	ACTCAATCTGGATGCCCCGTTGCTGGGCAAGGAAGCCAGTAATGTACTCTGAGTGGG	7120
Qy	114	-----	116
Db	7119	GAACAAGTCAGTATAGMAAAGCTGTTGTAGTGTGCTGCCAAGTTTCTTGCTGGCT	7060
Qy	117	-----	121
Db	7059	TCAAGTTATTAACAGTTTCCTCTACAGATAGCGCTTGTGATGTAGTCCAAAGTTGCC	7000
Qy	122	-----	123
Db	6999	AGAAATCTGCATCCAGCGCAGGTACTACTATACACAGAAATCGGGCTGGGATATTG	6940
Qy	124	-----	131
Db	6939	TCCCACTATGGCAGTCAAAATCCATCTTGATGGAGAGATTGAGGTTCTCAGAGCGGAAGG	6880
Qy	132	-----	133
Db	6879	CCGGTAGGATCATGAGCTGCGCCCAAGGATACCTCAGCAGGAACTCTGGGCGCCTCA	6820
Qy	133	-----	136
Db	6819	GAGTGACATGTGATGATCATGAGGATTCCTGGGCACAGCCCACTGTAGTCCAGTGTCA	6760
Qy	137	-----	143
Db	6759	TGCAGAGGTCAGGCAGGTGAAGGAAGCAGCAGTCGTATCTTTAGAAGCTGTTCTTACGT	6700
Qy	144	-----	145
Db	6699	TGACATCCAGTCCCCTCTGAAACACAACTGACCGGTTTCCAATGAAAGAAAGTGGC	6640
Qy	146	-----	147
Db	6639	TCCACTCCAGTGCATGTTCTCAGTTGTATTATAGGGTCCTCAGTGGCCAGCTGATGCA	6580
Qy	148	-----	149
Db	6579	GGTTTGCTTGTTCATATCCATATGCCAGTCCCATGGAAACAGACAGCGCTCTTATCCC	6520
Qy	150	-----	156
Db	6519	ACCAGGCAAAAGGTGGGCTGGGTCAGCTGAAGGCTTAGTCAAGAGGTCACACACTGAC	6460
Qy	156	-----	159
Db	6459	CAATCAGTGCCAGGCTGGATCCCAACATGGGCCCCCACCACCACTGTGTACTGGAAGATT	6400
Qy	159	-----	159

Db 6399 CCGAGTGGAAATCATGGTAAACTTGGAGTGGGGCATGTTCTTTCTACTGCCAGTTTAC 6340  
Qy 160 -----ThrGly----- 161  
Db 6339 CCCAGGGAAGCCCAAGTGCAGGATCTGACGTCCAGCGGAGCATGGCTGGCCACTCTGCT 6280  
Qy 162 -----Arg----- 162  
Db 6279 CAGTCCCGCAAGTGCAGCCATTAGCCCGCAGTCCCGGATCTCAACAGGTACCGTGGAT 6220  
Qy 163 -----Pro-----Glu----- 164  
Db 6219 AGTCTCTCATCCGAACACAGAAAGTTTGGACATTGCACTTGAGCATACGACACCACTGAG 6160  
Qy 164 ----- 164  
Db 6159 TGACAAGATCCATTCCTTTAGCAGGAAAGGGCTTCCAGGATCAAGTTCTCGAACCTGCT 6100  
Qy 164 ----- 164  
Db 6099 CTATCATGCTCGGGCCCATGAAGGATGATCTGTAGAGCCACCAAGCTCTAGCCCTG 6040  
Qy 165 -----Pro-----Thr-----Val----- 168  
Db 6039 CCAGGCTCCAAAGTGAAGTGCAGCGCGCATGGGTGTGTGCCATAGAGACGACGAGAGC 5980  
Qy 168 ----- 168  
Db 5979 GCTGATGATGATTTCAATGTTTTTGGGTTCGAAAGAGCGGTAGAGCTCCCAATTTTCC 5920  
Qy 169 -----TrpArg-----His-----Ile----- 172  
Db 5919 GAGCTGGCAATAGCTCTCCATGCTCTTTCGAGGGCAGCCACTTTGGCACTAGCAACT 5860  
Qy 173 -----Ser----- 173  
Db 5859 GCAGCCTTTTGGCACTCTCTTACTTTTATCCTTCATCCTGATGTTGTTATCATGAAGTT 5800  
Qy 174 -----Pro-----LysAla----- 177  
Db 5799 TCACCTCAAGATGTCATCCAGGAAACCCAGAAAGAGTGTGAACCTTTAGGAGTAAT 5740  
Qy 177 l -----Gly----- 178  
Db 5739 CAGGTGAAGAGGGCGAGGGCTTGAGAGCCCAAGCATGAGTCCCTCGATCGAGCCCT 5680  
Qy 179 -----Phe-----Val-----Ser-----Glu----- 182  
Db 5679 TTAGCAATTTGAACTCCACAGCCTCATCCAGAGTTCGAGAGAGTCACTACTGATAAG 5620  
Qy 183 -----Asp----- 183  
Db 5619 GAAACTCCACTGAGACTGATCCGAGGAAAGAACCAACCGATTGCGAGGGTCTGCA 5560  
Qy 184 -----Glu----- 184  
Db 5559 GCGCAGGGAAGGGTTCTGTGAAGGATCATCTTCTAGCTCAGGCAAGCTGCACCT 5500  
Qy 185 -TyrLeu-----Glu-----Ile-----Gln-----Gly----- 191  
Db 5499 CTACCTCTCAAGTTGAAGATGCTATTCCTCATTAAGCCAGCAGCAACTCGGGGAGT 5440  
Qy 191 e -----Thr-----Arg----- 193  
Db 5439 AAGCTGCAGTGAACCTCCATGCGGTTCAGCGACACACTCTCTGAGCCAGGTAATGA 5380  
Qy 194 ----- 194  
Db 5379 ACTGTGCTCAGCCAGAAAGTGTGTAGCTTGGAGTGTCTACCTCCAGGGTCAGGGTGA 5320  
Qy 194 uGln----- 195

Db 5319 GCAGCGCTAGGAGGAGATGACTCAGGAGATGGTCTTCTTGGCTCCCAAGTGGACTGTG 5260  
Qy 195 ----- 195  
Db 5259 GAGTGTTTAGTGAATGGGACTCAATAATCTCAGGAAACACAGTAGTCTCGTAAGAGGTCTC 5200  
Qy 196 -----SerGly-----Asp-----Tyr-----Gln----- 200  
Db 5199 GGCACCTAGAGTGGCCCTGCACATGTTGGTACAGATACATGTGATCTGGGGGGTCCAGA 5140  
Qy 200 u-----CysSerAlaSer-----Asn----- 205  
Db 5139 GTAAAGTCAGCCCTGCACC-----ACACTGAACCTCTAGAGAGCGGATGCTGTGTGATAG 5083  
Qy 206 -----AspVal-----AlaAla----- 209  
Db 5082 TGAGGGAGAGCATGGAGAGACCCAGCACTGGCGTGGGATGTCTAGGAGCCTTGCACAGG 5023  
Qy 210 -----Pro----- 210  
Db 5022 GCTGCATCTTCTGTGACTGATTTTACTAATGCAAGCACAGTCTTGTGAATCCCCACAG 4963  
Qy 210 ----- 210  
Db 4962 TGGAGGTCTCAGCACTACCAAGACAGTCACTGTGTCCAGTCTGTAGTCTTGAAGCACCAA 4903  
Qy 211 -----Val-----Val----- 212  
Db 4902 CCAGTGGGAAGAGTGAACAGGTTTCTATGTTTCCACCTTCAAGTCCACCTTCCACAGTA 4843  
Qy 213 -----Arg----- 213  
Db 4842 AGGTCACAGACTCCCAAGTGAAGCTTCTTAGAGACAGCTGACCTTTCAGATTGTGAA 4783  
Qy 214 -----Arg----- 214  
Db 4782 TCACCAAGAGAGAGACTCGAGACAGACACTGGGCACAGATGTCTGATATTCTACCTGAA 4723  
Qy 215 -----ValLys----- 216  
Db 4722 GTCTCTGANTAGTACAGTCAAGAAAGAGATTGGACTGGGTCTGGCAGAGCCAGGG 4663  
Qy 217 -----ValThr----- 218  
Db 4662 GCTGGTTATAACTCTTCCCTGTAGTGTGAAGGAATCCAGAACAGTGTCTGCCCCAACAT 4603  
Qy 219 -----Val-----Asn----- 220  
Db 4602 GCATATTAGGTGGATGTGGTCCCGCTGATGTGGAGTCACTGCCACAGCCAGCAGCA 4543  
Qy 221 -----Tyr-----Pro----- 222  
Db 4542 GATGATCTACAGTTAGCACTGCTCGTATGATGATATTTTGGCCGAGGTGCTGGTAGT 4483  
Qy 223 -----Pro-----Tyr-----IleSerGlu----- 227  
Db 4482 CCAGGAGATGGAATTGAACCCCAAGACCGTGGTGTATCTCCAAGCTGAATGGA 4423  
Qy 228 -----AlaLys-----Gly----- 230  
Db 4422 TGCTGACATTGGAGACTGAGGTGTGAAGATAATGGGAGCCAGGATCTGAGGGAGGTTC 4363  
Qy 231 -----Thr-----GlyVal----- 233  
Db 4362 TTTTCTTTCTTTTAAAGATCAGGTGAACCTGCTTCTTGGGTCTCCAGTCTCTAGCATAA 4303  
Qy 234 -----ProVal-----Gly-----Gln----- 237  
Db 4302 GGAGCCAGTGAAGAGAACTCTCTGGTGTCCGTAATGAATGATACAGGTGTTCAGAACTAGAG 4243  
Qy 238 -----LysGly----- 239  
Db 4242 AAGCTGAGAGTTCGATGTGTGCTCACCCTGCACATTTAGCCCTTGAAGGAGTTGAGGACAGAA 4183

QY 240 -----ThrLeu-----Gln----- 242  
Db 4182 TTGTTGGGCACTCTGGACAGCAACACCCATCTTCCATAGAGTTCAGTCTCATCT 4123  
QY 243 -----CysGluAlaSer-----AlaVa 248  
Db 4122 GTGCCATATCATAGTTTGTCTGTAAGCTTCGAAGCGGCACTGGTCTCATCAGCGTGGT 4063  
QY 248 1-----ProSerAla----- 251  
Db 4062 ACAGGAATGCACAGCTTCAGTGTCCAGTCAAGTCCGCTTTTGAAGTTCATAGACA 4003  
QY 252 -----Glu----- 252  
Db 4002 ACACCACACTGTGTCTCCATCTTCACCTTGACTTGGTCTGCAGCCGCTGGAGGAGT 3943  
QY 253 -----Phe-----Gln----- 254  
Db 3942 ATAGCCAGGACAGTGTGGTTCAGAAAGTTCTCAGTCAAACTCTGAACAGAACTGATT 3883  
QY 255 -----Tip----- 255  
Db 3882 TGGAAATCCGGCTGGGGATGACACAGTAGCTGACTATGGAAGAGACCTTCATGCAGCT 3823  
QY 255 ----- 255  
Db 3822 CAGCATGAGTGTCCACACATCCACAGTGACAGCCGCTCAGATGCCAACTGCTGACGCTGA 3763  
QY 256 -----Tyr----- 256  
Db 3762 CCGTAGGCGCAGTCCAGGGCCAGTGAGAGCTCTACCAGACATGTATCTCCAGCTGAC 3703  
QY 256 ----- 256  
Db 3702 CACTCTTCAGGACTTCGCTATTGATCTTTGATAGTTTCACTTTACAGATGAGACTCTTCC 3643  
QY 257 -----Lys-----Asp-----Lys-----Arg----- 261  
Db 3642 CATCACTGTCCAAAGAAATCTGCTTACTGATCTGGATGTGGTGTGCCAAGGACTCAGAGG 3583  
QY 262 -----Leu-----Ile----- 263  
Db 3582 TAGCCACCTTAAGAACCATTGATGTTTATGGCATCTACATGAATGGAGAATAGTTGGCAGA 3523  
QY 264 -----GluGly----- 265  
Db 3522 AGATCTTCAACAGGATGGCTGAGGAGCAGTTCTCTTTTGCTCCACCTCTGTGTCTGAG 3463  
QY 266 -----Lys----- 266  
Db 3462 AGAATGGGGCAGACAGGCTAGAAACCTCTGTAGATCTGTCTGTATGCGCACTTCTCCAA 3403  
QY 266 s-----Lys-----Gly----- 268  
Db 3402 AGCAATGCCCATAGTTTGGCAGATCATGCTAGAGAGTTTGTCTGGAAATCCCAAGT 3343  
QY 269 -----Val-----Lys-----Val----- 271  
Db 3342 TGTCAATTTCCACCGTCTGCTGTCTGTCTGCTGAACTTAAGACTGACATCTCTGGATCCAA 3283  
QY 271 ----- 271  
Db 3282 AAAATCGAAGGACCAATCTTTAGCTCTGCTGCAACTTGGCTGACACACCTGGTGG 3223  
QY 272 -----Glu----- 272  
Db 3222 CCACCGGACCAAGCCACCGGCTTAGGAAGAGTGCCTAAGCGCAACCGACGACGA 3163  
QY 272 ----- 272  
Db 3162 CCAACAGCGCGGAGAAATAGAGGCAATTTAGTCCGGGTCCGGCCCGGCGCTGGCCCGCA 3103

QY 273 -----AsnArgPro-----Phe----- 276  
Db 3102 CCCCCCGCATGCGGGGCCCTGACGCGGAACGCCCGCTCTCGAGTTCTGTGGAAGTTG 3043  
QY 277 ----- 277  
Db 3042 ATGTTTACATATTTAGTGGCCATTCCTATTCTCTTTTGTGAATGCGCTTTTATATCCT 2983  
QY 277 u-----Ser----- 278  
Db 2982 TGTCTCTCTTATTTTGAATGTTTCTTATTATTGTAAAGATTCCCATCTAACCTTA 2923  
QY 279 -----Lys-----Le 280  
Db 2922 ATTTCTAAATCTTATTGGTTATATTATACAGATGCATCCAGCATGTCTGTGTTTT 2863  
QY 280 uile----- 281  
Db 2862 AATTTTGTAGTGGGCGCACATGCAGGTAAAAATTTCCCTTCTATTACTAAATCTTTAGG 2803  
QY 281 ----- 281  
Db 2802 GATTTTCATTCCAAATATCAAATAATTTAATGTTTATAAATCTACTTAGTTTTCTATT 2743  
QY 281 ----- 281  
Db 2742 TCTTCTTGAGTTACTTTTGGTAGTATATGTTTTTCAATCAAAATGTTTCTACTTTTTAAA 2683  
QY 282 -----PhePheAsn----- 284  
Db 2682 GTTTAAATTTTATGGCTTAAATTTGACTTAATTAATGCTAAATTTTTTTTTTAATTTCTA 2623  
QY 285 -----ValSer----- 286  
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QY 301 -----LeuGly----- 302  
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QY 302 ----- 302  
Db 2082 GGAGAGAGATGGGCACTGTCTCTTTTCTGCTTATAGGTTACAGAGCAAGATTCGTCA 2023  
QY 303 -----His-----Thr-----Asn----- 305

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Db 2022 ACTCCATATAGCAGCAGCAATCTTTGTTTCAGTGTGTATCCCTAGTGCCTTAGA 1963
QY 306 -----Ala-----Ser-----Ile----- 308
Db 1962 ACTGTGCTGGCACAATAATACATGCTCAGTAAATATTGTAGATGAGAAAAGCTTTCAA 1903
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QY 311 -----PheGly----- 312
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QY 315 -Ala-----Val-----Ser----- 318
Db 1722 GGCAGAACTGTGAGAGAAAGATGTGATCAGAGAAATATTGCTCTGAAGAGAGAC 1663
QY 319 -----ValSer-----Asn----- 321
Db 1662 AAAAATCAAGCTGAGGGTCTGGGAGTCACAGATGGGATCGCTCTCCAGACAATCATTCG 1603
QY 322 -----Gly----- 322
Db 1602 AAGCACCAGCCCTGGGATCGGAGCAAGACGCTCACCGAGCTAGGACCTAGAAGCCCTCC 1543
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Db 1482 GAGGCTCAGGAATGTGTGATTTATGCTAGTACGAGGAGTCAACCTCATACATTGAG 1423
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Db 1422 GGAGAAGCAGCGGAGACGCGCACGAGATTCGCCCATCTCTTTGATATAATTTTAGA 1363
QY 329 -----CysVal----- 330
Db 1362 TTGAGATTCAAGATTAAATCCGAGGGGAAAACACTTTATGAGGCTGAAGCTGTGTGTTG 1303
QY 331 -----Trp----- 331
Db 1302 CCAGAGACAGGTTATGAGCTATCAATGCAATTACATTAAGACAGATTATATCTGGGCAA 1243
QY 331 ----- 331
Db 1242 ATTGAGCATTAGAGGTGAGATCAAGAAAACGGCTCTGATCTCTTTTCCCTCTTCT 1183
QY 332 --Leu--LeuProLeu-----Leu----- 336
Db 1182 CTCTCCCTCTCCCTCTCTCTCTAAATTCGAGTTCGTAGTTCCTTCCAAATTCGAGGACCA 1123
QY 337 -----ValLeuHis----- 340
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QY 340 eu-----Leu-----Leu----- 342
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RESULT 22  
AK090138

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LOCUS AK090138 10481 bp mRNA linear HTC 20-SEP-2003
DEFINITION Mus musculus 7 days embryo nullipotent stem cell CRL-2070 NE cDNA,
RIKEN full-length enriched library, clone:G431005B01 product:igene
e1 protein, full insert sequence.
ACCESSION AK090138
VERSION AK090138.1 GI:26354968
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
9279253
PUBMED 10349636
REFERENCE 2 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes
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20499374
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Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hayada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
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20530913
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REFERENCE 4 The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
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Group Phase I & II Team.
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of 60,770 full-length cDNAs
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6 (bases 1 to 10481)
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FUKUDA, S., FURUKAWA, K., HIRAKAWA, T., HARA, A., HASHIZUME, W.,
HAYASHIDA, K., HAYATSU, N., HIRAMOTO, K., HIRAKAWA, T., HIROZANE, T.,
HORI, F., IMOTANI, K., ISHII, Y., ITOH, M., KAGAWA, I., KASUKAWA, T.,
KATO, H., KAWAI, J., KOJIMA, Y., KONDO, S., KONNO, H., KODA, M.,
KOYA, S., KURIHARA, C., MATSUYAMA, T., MIYAZAKI, A., MURATA, M.,
NAKAMURA, M., NISHI, K., NOMURA, K., NUMAZAKI, R., OHNO, M., OHSATO, N.,
OKAZAKI, Y., SAITO, R., SAITO, H., SAKAI, C., SAKAI, K., SAKAZUME, N.,
SANO, H., SAKAKI, D., SHIBATA, K., SHINAGAWA, A., SHIRAKI, T.,
SOGA, Y., TAGAMI, M., TAGAWA, A., TAKAHASHI, F., TAKAKU-AKIHARA, S.,
TAKEDA, Y., TANAKA, T., TOMARU, A., TOYA, T., YAEUNISHI, A.,
MURAMATSU, M. and HAYASHIZAKI, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
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Db 2165 CTGGGATCAATTTTAAACCGAATAACATATAGTGAAGGAACCTTTACATACATGATTAAAT 2224  
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Db 2225 TCAAAAATCTTGAATGAGAAGATTATCTCAATTATCCAGCAGACCCAGTGAATCA 2284  
QY 49 GlnGly-----  
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QY 52 -----  
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QY 58 -----  
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QY 60 -----  
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QY 70 -----  
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Db 2885 GCATCTGTAATAATAATACCAATAAGATTTTAGAAATTAAGGTTAGATGGGAACTCTT 2944  
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QY 76 -----  
Db 3005 AAGAAGAAATAGGAATGGCCACTAAATATGTAACAATCAACTTCCACAGAACTCGAGAG 3064  
QY 77 -----  
Db 3065 CGGGCGGTTCGGCGTCAGGGCCGGCATGGCGGGGTGCGGGGCGAGCGCCGGCGGAC 3124  
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AspLysTrp-----  
Cys-----

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Cys-----Ser-----  
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ValGln-----Thr---Asp-----Asn-----  
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QY 122 -----  
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Pro-----Lys-----  
Db 4322 CCAAGGAGCCAGTTCACTGTATTTAAACAAAGAAAGAAACCTTCCCTCAGATCCT 4381

QY 125 -----ThrSer----- 126  
Db 4382 GGCTCCCATATATCTTCAGCACCTCAGTCTCAAATGTCAGCATTTCCATTAGCTTGAGAGA 4441  
QY 126 ----- 126  
Db 4442 TACACCACCGTTTGTCTTTGGGGTTCAATTCATCTCCCTGGACTACCCAGCACCTCCGGCC 4501  
QY 127 -----Arg-----Val--HisLeu-----Ile----- 131  
Db 4502 ACAAGTATCCATCAGCAGAGAGTGCTAACTGTAGATCATCTCTGCTGGCGTGTGGCAG 4561  
QY 132 -----ValGln----- 133  
Db 4562 TGAATCCCATTCAGCGGCGCACCATCCACCTAATATGATGTTTGGGGCGNAGCACT 4621  
QY 134 -Val-----Ser-----Pro----- 136  
Db 4622 TGTTCGGATTCTTCACACTACAGGGAAGTTATAACAGCCCTGGGGTTGTCCAGCAC 4681  
QY 137 -----LysIle-----ValGluIleSerSe 143  
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QY 181 -----Ser--Glu-----Asp----- 183  
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RESULT 23
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DEFINITION genomic survey sequence.
ACCESSION AY405009
VERSION AY405009.1 GI:39760983
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 9744)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 9744)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferrier,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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gene
ORIGIN
Alignment Scores:
Pred. No.: 8,73e-13 Length: 9744
Score: 1672.90 Matches: 270
Percent Similarity: 11.31% Conservative: 64
Best Local Similarity: 9.14% Mismatches: 9
Query Match: 69.47% Indels: 2611
DB: 29 Gaps: 263

US-10-017-084A-523 (1-344) x AY405009 (1-9744)
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QY 5-----Gln-----5  
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QY 6-----Pro-----6  
Db 948 ATGGATGTTTGAACCCCAACCAATCGACACACTTGGGGCTTATTCTCTGACACTGTAGA 1007  
QY 7 Lys-----Methis-----9  
Db 1008 AAATCGAGAAATTCCTGAGCTAGCCAGGAGATGCTGCAAGCTCGGTGGATGTT 1067  
QY 10-----Aen-----Ser-----IleSer---13  
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QY 27 Gln-----Gly-----28  
Db 1368 CAGAGAAGCGTTGAAAGGGAGATGTTAAGAACAGCAGCGTGGATGTTTGAACACACAGCC 1427  
QY 29 Val-----Pro-----Val-----31  
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QY 32 ArgSer-----GlyAsp-----Ala-----ThrPhe---38  
Db 1488 AGAAATGTCAAAGGTGGGTGAGTAAGCAAGGTGTTTATTGAAACCCCACTTTGGA 1547  
QY 38-----38  
Db 1548 GAAATCAAGAGTCAGAAGGTGATCATTCATTGAAAGGAAATAATAGGTACAGATGT 1607  
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QY 56-----ArgCys-----57  
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QY 58 Thr-----Ile-----AspAen-----Arg-----62  
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QY 63 ValThr-----Arg-----65  
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QY 66---ValAla-----67  
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QY 112 ---Pro---Tyr-----Thr----- 114  
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QY 130 Leu-----  
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QY 130 ----- 130  
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QY 162 -----Pro-----Arg----- 162  
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QY 163 ----- 163  
Db 5145 TCTTCCAAAGCCCCCAAGGCACTGTAAAGATTGTCTATAGATTGTCTAGAACAAAACAATGA 5204

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QY 168 -----Thr-----168
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QY 168 -----168
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QY 194 Glu-----GlnSer-----196
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QY 213 -----ArgArg-----214
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QY 221 ---TyrPro-----222
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QY 222 -----222
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QY 223 -----Pro-----223
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QY 224 ---Tyr-----IleSerGlu-----AlaLys 229
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QY 230 -----Gly-----Thr-----Gly 232
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QY	236	-----Gly-----Gln-----	237
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QY	238	-----Lys-----GlyThrLeu-----	241
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QY	242	-----Gln-----	242
Db	7605	TGAAGAAAAACAGAAACATCTGAAGATAAATCAGACCAAGGTCGTCAAGCAAAAGGT	7664
QY	243	-----Cys-----Glu-----Ala-----	245
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QY	246	-----Ser-----AlaVal-----Pro-----SerAla-----	251
Db	7725	TGAAAGTAAAGCTGAACATAAAAAATTCGCCCCAGCCATATAATAGTCTCGAGGAAGAAAA	7784
QY	252	-----Glu-----Phe-----	253
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QY	254	-----Gln-----	254
Db	7845	GCAAGAGATTACACAGAACCAATCTTTCTTCTGTGAAGAAATCCCGCGGGATGA	7904
QY	255	-----Tyr-----Lys-----Asp-----	258
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QY	258	-----	258
Db	7965	TTTGTGCGAGTGAACAGTTTGAAGCAGAGCCAAATAAAGTGGCCTTAAACATTCA	8024
QY	259	-----Lys-----ArgLeu-----IleGlu-----	264
Db	8025	GACACTATTAATACTATCCCGAGGATGGCTGATAAGTGAAGATAAGAGAGATATGCAGT	8084
QY	265	-----Gly-----Lys-----Lys-----	267
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QY	274	-----	274
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QY	275	-----PheLeu-----	277

D	b	8445	CCACCGTCACCAACTTTTATCACAATAGAACTCTACTGCCGACGACGAACAGAAAACCCTAC	8504
Q	y	278	-----Ser-----Lys-----Leu-----	280
D	b	8505	TAAGAACGAGCTTTCTCAGTCCCCTAAAAAGGACAGTTATGTGGAAACCCCCACCAAGAAG	8564
Q	y	281	-----Ile-----Phe-----Phe-----	283
D	b	8565	GCCCATGTGCMAAATCTGAATTACAGAGCAAAACACTTCCCTTCTCCACCAGGAG	8624
Q	y	283	-----	283
D	b	8625	TGCTCTGAACAACCTTGACACTCAAGACACCACTGCAAGATTATCCAAGGGGCCAT	8684
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Q	y	289	-----Asp-----Tyr-----Gly-----	291
D	b	8745	TCCTGCAACACTTCGTCTCAAATTAAGATAGAACTCGTGGTAGGACTCTCCACCTAC	8804
Q	y	292	-----Asn-----Tyr-----ThrCys-----Val-----	296
D	b	8805	AATCACAATACCAGTAATAATCATGCTGCTAGTGGTTCTCTCAGAGAATCTGTGGA	8864
Q	y	297	AlaSer-----Asn-----	299
D	b	8865	CGCTCAGAGGAATCAGGAAAGTGAGAGAGACTATTATGTTCATAAAGATGGACT	8924
Q	y	300	LysLeu-----Gly-----His-----Thr-----Asn-----	305
D	b	8925	AAATTCACCTGATCACAATGTCGCCGACACTGAAAGTTATGATGCAGTTGAAATCATCG	8984
Q	y	306	-----AlaSer-----Ile-----Met-----Leu-----PheGly---Pro	313
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Q	y	314	-----Gly-----AlaVal-----	316
D	b	9045	AACGTTCAAATGGCTGAAANNTTCGTGAATGACCTGAAANTGAANTAAACAGATGGTT	9104
Q	y	317	-----SerGluVal-----Ser-----	320
D	b	9105	CAGGGAATTTGAGCATGCGCCAGTTTCTGAAGCAAAAGTCAAANTAGAAGTTTTATGCAA	9164
Q	y	321	-----Asn-----Gly-----	322
D	b	9165	GGGAGAAACAAACATAACAAAGAAAGTGTACATTTTGTGAAGGAGGAATTTGG	9224
Q	y	323	-----ThrSer-----Arg-----	325
D	b	9225	ATTAACATCTTAGGAAACACGAGTTTACAGACTTTCTTGCAAAACATCTCAGAGAACT	9284
Q	y	326	-----Arg-----Ala-----	327
D	b	9285	GCGAGAAAGATTCTGTTAAGCAGCGCCAGGATCTGCTCTGAAACCAAGTCTCTAAGTGA	9344
Q	y	328	-----GlyCys-----	329
D	b	9345	ACATTTCTAGGCATGGATGCATTTGAGAGTCAAAATGTGTAGTCGAAGATGAAAAACCTC	9404
Q	y	330	-----ValTrpLeu-----Leu-----Pro-----	334
D	b	9405	TTCATCACATAGCTCAGAAGCTGGCAATCTGGCTGTGACTTCAAGCATGCCCAACCAAC	9464
Q	y	335	-----LeuLeu-----	336
D	b	9465	CTATGAGGATGTCATTGCTGGACATATTTTAGATATCTCTGATTACCTAAGAGTAAG	9524
Q	y	337	-----Val-----	337
D	b	9525	AAAAAATTTTCAAGACCTGGCAAGAGAGTGAAGAGATTTTTTAAGGCGCTGGGATATGC	9584

QY 338 -----Leu-----HisLeu-----LeuLeu 342  
 Db 9585 AACCCGAGATGCTTCTGCAACTGAGATGAGAACCACCTTCCAGAGGAATCTGCATTAT 9644  
 QY 343 Lys -----Phe 344  
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RESULT 24  
 AK090135/c  
 LOCUS  
 DEFINITION  
 SR-4987 cDNA, RIKEN full-length enriched library, clone:G431004D19  
 product: fibronectin 1, full insert sequence.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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 Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N.,  
 Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N.,  
 Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T.,  
 Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,  
 Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,  
 Muramatsu, M. and Hayashizaki, Y.

TITLE  
 JOURNAL  
 Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of  
 Physical and Chemical Research (RIKEN), Laboratory for Genome  
 Exploration Research Group, RIKEN Genomic Sciences Center (GSC),  
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 Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,  
 URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,  
 Fax: 81-45-503-9216)

COMMENT  
 cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in RIKEN  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.  
 Please visit our web site for further details.  
 URL: http://genome.gsc.riken.go.jp/  
 URL: http://fantom.gsc.riken.go.jp/.

FEATURES  
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AUTHORS	Carpten,J.D., Makalowska,I., Robbins,C.M., Scott,N., Sood,R., Connors,T.D., Bonner,T.I., Smith,J.R., Faruque,M.U., Stephan,D.A., Pinkett,H., Morgenbesser,S.D., Su,K., Graham,C., Gregory,S.G., Williams,H., McDonald,I., Baxevasis,A.D., Klingler,K.W. and Lande,G.W.					
TITLE	A 6-Mb high-resolution physical and transcription map encompassing the hereditary prostate cancer 1 (HPC1) region					
JOURNAL	Genomics 64 (1), 1-14 (2000)					
MEDLINE	20175426					
PUBMED	10708513					
COMMENT	Contact: Carpten JD Cancer Genetics Branch National Human Genome Research Institute/National Institutes of Health Bldg. 36, Room 3D04, 36 Convent Drive, Bethesda, MD Tel: 301 435 5626 Fax: 301 435 5465 Email: jdc@nhgri.nih.gov Class: shotgun. Location/Qualifiers					
FEATURES						





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Db 6472 AATTTTAAGTAATTTTAACAGTATGAACACATGTGGAGCTTACAGAAAAGTTGCAATG 6413  
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QY 312 -----Gly----- 312  
|||  
Db 6412 TGATAGGAGAGATGTTTCTCTCTGAGCCATTTAGGAATAAGTTACTAATCAATGAGTT 6353  
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QY 313 -----Pro----- 313  
|||

Db 6352 CCATCACCCCTGAATAGTTTAAATGTTGCTTACTACAGATAAGGATAAATCTGCTACTATC 6293  
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QY 314 -----Gly-----AlaVal-----Ser 317  
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Db 6292 CACAATATAAGCATCACATCAGGATATTAGCAATTGATACATTACTATGACCAACTTCA 6233  
|||  
QY 318 Glu-----Val-----Ser 320  
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Db 6232 GAGCGCATTCATATTTCACAGTCTTCTGCTGGCATCTTTTATCTGTCAGTGAACAGT 6173  
|||  
QY 321 -----AsnGlyThrSerArg-----Arg----- 326  
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Db 6172 TGGTGAACATCAATGGA-----AGAATTCAGTCAGATCCCATGTTGCTTTCAGTTG 6119  
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QY 327 -----AlaGly----- 328  
|||  
Db 6118 TCATGTTTCTTTAGTCTTCTTCAGTCTGGAACAGTCTCTGCTCTTCTGCTGCTAAT 6059  
|||  
QY 329 -----Cys 329  
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Db 6058 CTTTACCATTTTGAAGATGACAGATGGCTATACATTTCCTTGGCAATTTGAGTTGTC 5999  
|||  
QY 330 -----Val----- 330  
|||  
Db 5998 CTGTCACCTCTTCGTGATTAGATTTCAGGTGCTGCTATGCGAGATTTATCACAGAAGC 5939  
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QY 331 -----Trp----- 331  
|||  
Db 5938 AATGCTACATTTCTTTGCAATTTACCAAGTGGGCAATTTGCTTCTGCTTCTGCTGTA 5879  
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QY 332 -----Leu-----LeuPro----- 334  
|||  
Db 5878 GAACACAGTTTGTATGACTTAGTCTGCCAGGTTTCTCTACAAAGCTTACTCTTTTCC 5819  
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QY 334 ----- 334  
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|||  
QY 335 LeuLeuVal-----Leu----- 338  
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Db 5758 TTATTAATCTATCTATCTATTTTACATCAATGAGTCAATTTGCTTCTATATTATTCAATG 5699  
|||  
QY 339 ---His---LeuLeu-----Leu-----LysPhe 344  
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Db 5698 GATCAATATCTGTTGCCAACATTTATTATTGAATGTTT 5660  
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RESULT 26  
AQ839854 14771 bp DNA linear GSS 31-MAR-2000  
LOCUS 260L13-C54 CITE Homo sapiens genomic clone 260L13, genomic survey  
DEFINITION sequence.  
ACCESSION AQ839854  
VERSION AQ839854.1 GI:6652486  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Carpten, J.D., Makalowska, I., Robbins, C.M., Scott, N., Sood, R.,  
Connors, T.D., Bonner, T.I., Smith, J.R., Faruque, M.U., Stephan, D.A.,  
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TITLE A 6-Mb high-resolution physical and transcription map encompassing  
the hereditary prostate cancer 1 (HPC1) region  
JOURNAL Genomics 64 (1), 1-14 (2000)  
MEDLINE 20175426  
PUBMED 10708513  
COMMENT Contact: Carpten JD  
Cancer Genetics Branch  
National Human Genome Research Institute/National Institutes of  
Health



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Db 5415 TTTCATCCAAATTTGGAAGCTCCCTTATTGCTGCGCTTCTCCCTCATCACTACTCTGGTAAG 5474
Qy 72 SerThrile----- 74
Db 5475 AGTACAATTTAGGCTCCTAAATTTTACAACATAGTGTAAAGCTCTTTGCGCTGTAATGT 5534
Qy 75 -----LeuTyr----- 76
Db 5535 GCTATTATTATGAATTCCTCTTTACCTATATACTATTGAAAATATACATTTGGCTGGGTG 5594
Qy 76 ----- 76
Db 5595 AGTGGCTCATGCTGTATCCAGCACATTGGGAGGCCAGCGGGTGGATTGCTCAAGC 5654
Qy 77 -----Ala-----GlyAsnAsp-----Lys----- 81
Db 5655 CCAGGAGTTTACCAGCCTGGGCAACATGGGGGAACCCCTGTCTCTACAAAAAACAGTGGG 5714
Qy 82 -----Trp-----CysLeu-----Asp 85
Db 5715 TGTGGTGGCAGCGACCTCTAGTCAGTCTCAGCTGCTTGAGAGGCTGAGGTGGGAAGAT 5774
Qy 86 -----ProArg----- 87
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Qy 88 -----Val----- 89
Db 5835 TGGGTGACATAGTGAGACCCTGTCTCAATAAACAACAAAAACAACTTTTCAGAAC 5894
Qy 90 Leu-----Leu-----Ser----- 92
Db 5895 TTAGGAATAGAGGCGAACTTCAACTGTGACAGCAGCATCTACAAAAAAATCTATAGCT 5954
Qy 93 -----AsnThr----- 94
Db 5955 AACATTTAATTTGTAACACTTTCAGTTCCTCCTGTGATTGTGAACAAGTATGCTCTCAT 6014
Qy 95 -----Gln 95
Db 6015 ACTTATTCAACATGGAATTTCTAAACAAGAGAAGAAAAAATGATACAGATCAA 6074
Qy 95 ----- 95
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Qy 98 -----Tyr-----Ser----- 99
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Qy 100 -----Ile----- 100
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Qy 106 -----AspVal----- 107
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Qy 108 -----TyrAsp----- 109
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Db 6495 AATAAAGGAAACATATTTTAAAAAGGAGACATTTAAGAAAAAACCCAGCTAATTTTCATACT 6554
Qy 109 ----- 109
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Qy 112 -----Pro-----TyrThr----- 114
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Qy 114 ----- 114
Db 6735 TCTTGTGGCTCTGGCAATTTTGGCATTCCTTAACCTTTTGGATGCATCCTCCAGTCTT 6794
Qy 115 -----CysSer----- 116
Db 6795 TGCTCCATCTTTTGTGTTTTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 6854
Qy 117 -----ValGln----- 118
Db 6855 GCTGGAGTGCAGTGGCATAATCTCAGCTCACTGGGCTCTGCTCCAGGTTCAAGGA 6914
Qy 119 -----Thr-----Asp----- 120
Db 6915 TTCTCTGCTCGGCCCTCTGAGTAGTGTGAGACTACAGGCATGTACCACCATGCCAACT 6974
Qy 121 -----Asn 121
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Qy 125 -----Thr-----SerArg-----Val----- 128
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Db 7155 TCTTTTCTGCTAAGGACACCTCTCATTTAGGATTTAAGACCACCTTAATCCAGGATGA 7214
Qy 129 -----HisLeu----- 130
Db 7215 TTTTCATCTCAAGATCCTTAATTACATTTGCAAGACCCCTTAATCCAAATAAGGTCACTT 7274
Qy 131 -----IleVal----- 132
Db 7275 CTGAAGTCTGGTAGACATGCTTTTGGAGGCCACTATTCAATTCATTATAGTACACTCT 7334
Qy 133 GlnVal-----Ser----- 135
Db 7335 CAGATCCCTCAAAATTCAGGTCTGTCCCATCATGCAAAATACCTTACTTCAATCCAAATC 7394
Qy 136 -----Pro----- 136
Db 7395 CCCCTGAATCAACCTATTCCAGCATCAACCTGTPACATCTAATACCTCTTGTAAATATTT 7454
Qy 137 -----Lys-----IleVal-----Glu-----Ile 141
Db 7455 TAACTCAAAAAGTCCCAATCTTATCTAATTCAGGTATGGGTATGATCTCTGGGTATGATC 7514
Qy 142 -----SerSer-----Asp----- 144
Db 7515 CATCTAGGSCATAAATTCCTTTCTAGCTGTAGACCTGTGGACTAGAAAACCAACTATCTG 7574
Qy 144 ----- 144
Db 7575 CTCCTTAAATACAAATGGTGGGACAGCACTGGATAGCAATCCCAATTCCTCAAAAGGAGAA 7634
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Db 7635 GGAGGATGAATAAAGGTATCACAGATCCTAAACAAGTTTCAAAACCCAGCAGAGAAATC 7694  
QY 148 -----Asn 148  
Db 7695 CCATTAGGTTTGAAGCTTGAGAAATACCTCTGCAGCTTAATCTCTGCTCTCCAGAAT 7754  
QY 149 -----GluGly----- 150  
Db 7755 CAGTGTCCACACTCTGGGTCCATGGAGGCTCCTTTGGCTGTCCAGAGGGGTACCTCTC 7814  
QY 150 ----- 150  
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QY 150 ----- 150  
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QY 151 -----AsnAsn----- 152  
Db 7935 GAATCTAACACCTTTTTCATTTTGTATAGTCTCAGTCTCTTTTATTTCTAAGCCAGCA 7994  
QY 152 ----- 152  
Db 7995 ATGTTTCTGCTGTATTAACATCTCAAAATCCTTGTCTATCTCCCATGTCTCATCCCATG 8054  
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Db 8055 GAGGTCCATGCCATTAGACAGAGAGATCTGTCTTGATAGATAGACCTATCTATCTCT 8114  
QY 157 -----Cys----- 157  
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QY 158 -----Ile-----AlaThrGly----- 161  
Db 8175 CATCCATGAGTCACACACCTAAATCTCTTCAGCAACAGTTGTCCAGTCAGTCCCTTGGCC 8234  
QY 162 -----ArgProGlu-----ProThrVal-----Thr----- 168  
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QY 169 -----Trp----- 169  
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QY 170 Arg-----His----- 171  
Db 8355 CAATTTATCTCTTCTCTCTCACATTTTACTCTAAGCAGCAAGAGAAATCAGGCTGGCC 8414  
QY 172 -----IleSer-----Pro-----Lys----- 175  
Db 8415 TTCAACACTTGTTACTTGAAATCTCAGTTAAATATCCAAAGTTTCATAGCTTANTAAGTTC 8474  
QY 175 ----- 175  
Db 8475 GTTTTACCCACAGTAAACATAACTTAAGTGGTNTTCTGGTNTGNTGGTTGA 8534  
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Db 8535 GACTGAGTCTCGCTCTGTCCACCGGCTAGAGTGCAGTGTGCTATCTCAGCTCACTGCA 8594  
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Db 8595 GCCTCGCCTCCAGGTTCAAGCTATTCTCCTGCTCTCAGTAGTGTGGATTACAGCG 8654  
QY 178 -----GlyPhe----- 179  
Db 8655 AGCGCCACACGCCAGCTAAATTTTGTATTTTGTAGTAGAGTTGAGGTTTCCACCATGTTG 8714  
QY 180 -----ValSer----- 181

Db 8715 GCAAGGCTGTCTCGAACTCGAACTCCTGATTTCAAGTGATCCATCTGCTTGCCTTCC 8774  
QY 181 ----- 181  
Db 8775 GAAGTCTGGGATTACGAGGTGTGAGCCCGCTGCTGGCTGTAGTTTCTGTTTATATGA 8834  
QY 182 Glu----- 182  
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QY 183 -----Asp----- 183  
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QY 184 ----- 184  
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Db 9075 TAIGTTTTAAAGGCTCTCAAAATATTAAAGTACTATCTAGAAATAGTAAATCTAAATTTCT 9134  
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Db 9135 TTATTTCTTAATGTTAGAAATGTTACAGTTGCAATTGAAATGTAGGTCCCATTTATCAGTTT 9194  
QY 190 Gly----- 190  
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QY 191 -----IleThr----- 192  
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QY 192 ----- 192  
Db 9315 ATTATTAAATGTCAGTTTAAATTTGTTCTGAAAGCTTTTGGGTAAATCTTTGGAATAATTGAT 9374  
QY 193 -----Arg----- 193  
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QY 196 -----SerGln----- 197  
Db 9495 CAGACTGGAGTGCAGTGGGTGATCATAGTCTTACTGCAGCCTTGAACCTCTGGGCTCAGG 9554  
QY 197 Asp----- 198  
Db 9555 GGATCCTCCCAATTTAGTCTTCTGAGTGGAACTATAGGTGTCTTACCATCACACCTG 9614  
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QY 200 ----- 200  
Db 9675 GGTGTCTCAAACTCTGGCTCAAGTATCCTCCTCTTGGCTCCCTCCCAAGTGTCTG 9734  
QY 201 -----Cys----- 201  
Db 9735 GAATACAGGTGTGAGCCATGCACTGGCTATCATTTCTTAAATGAGATTGTTTTT 9794  
QY 202 -----Ser-----Ala----- 203

Db	9795	ATTTTAAATCCCTGTGTTCAATATGTTGCTTAGTCCTTTTGAGAGTAGTTTAAGAGCTAA	9854
QY	204	-----Ser--	204
Db	9855	CAATGGGGTAAATTCATAAATTATTACTTTAAAAATGCTTTGAATAAAATAGTATTCAGT	9914
QY	205	-----Asn-	205
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QY	205	-----	205
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QY	206	---Asp---	206
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QY	207	-----ValAla-	208
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QY	209	-----Al	209
Db	10155	ACTTTGGAGGCAGAGCAGGAGGATCACTTGAGACTAGGAGTTCAAGACCAAGCCCTGGGC	10214
QY	209	a-----	209
Db	10215	AACATAATGAACCCGTCTCTATATAAAAGAAAAATAAAATAGCTGGGTGGTGGTG	10274
QY	210	---ProValVal-	213
Db	10275	CACACCTGTAGTCCCAGTTACTAGCAGCGCTGATGTGGGAGGATTCCTTGAACCCAGGAG	10334
QY	214	---Arg---	215
Db	10335	TTGAGGCTGCCAATCAGCCANGATCACTGTGTTCACTCTAGCCTGGGCAACCCGTGTTTC	10394
QY	216	-----Lys-	217
Db	10395	AAAAATAAATAATAATAAATAAATACTAAATAATAATTAACATTTTCTGTGCCATAGC	10454
QY	218	-----Thr-----ValAsn-	220
Db	10455	TAGTTGTTAACATTTTAAATGATTAATAATTTTAGGTGTATGAACCATAGTATATTTAAT	10514
QY	221	-----Tyr-	221
Db	10515	CAITTCATTGTGGTTCGTTTATAAGTTTTTTTAAAGTTTATTATTATGTTTCATGATAG	10574
QY	222	-----Pro-----	222
Db	10575	CACGTCCATTATTATGTGGCGGTGGATGGAAGTAAGCAGTAGCTGTTGTCCCGCTAA	10634
QY	223	-----Pro-----Tyr--IleSer-	226
Db	10635	GTITACCTTCCAGAAATGAACTGTAGTGTCTTTGATGGCAGTAGCTGTTGTGCAGT	10694
QY	227	Glu--AlaLys-	229
Db	10695	AGAGCTGAAGAAAACAAGGAATGAAAGAGATAGCTGTTTCCCATTTAGCCTTGAGAA	10754
QY	230	-----Gly-----Thr-----GlyVal-	233
Db	10755	TTCTTTTTAGGTAGTGACAGCAATATGTTCTTGACCTTCAGTCCAGGAGTGTCTAAGGA	10814
QY	234	Pro-----Val-	235
Db	10815	TCCACAAATACAGTCATCCGTCTGTATCCATGTTTCTGTATCCCTTGGATTCAACAGACTG	10874
QY	236	-----Gly-----GlnLys--	238
Db	10875	CAGGTGAAAATTAATCTCTAAAGGGGAAAAAAGAAAAACAGTAAAAACAGTTCAAAATA	10934

QY	239	-----GlyThr-----Leu-----	241
Db	10935	ATACAAATTTTGGCCAGGCAAGGTAGCTCATGCCCTATAATCCAGCACTTAGATGGATG	10994
QY	242	-----Gln-----	242
Db	10995	GGTCAC TTGAGCCAGATGTTTGAGACCGAGGCTTGGCAACATGGTGAGACCCCTGCTCTTA	11054
QY	242	-----	242
Db	11055	CAAAAAATACAAAAATTAGCCGGCTTGGTGTGGCACACCTATAGTCTCAGTTACTCAGG	11114
QY	243	-----Cys-----Glu-----	244
Db	11115	AGGTTGAGTGGGAACATCACCGAGCCCTGGGAGGGTTGAGCGTCGAGTGAGCCCTTGATT	11174
QY	245	-----Ala-----Ser--	246
Db	11175	GGCGCTTTCATTTCCAGCATTCCTGACAGCGCATACCCCATCTCAGATNATNATAGTAA	11234
QY	247	-----AlaVal-----	248
Db	11235	TACAAATTTTAAAGATCGCACTCTAGCACTAGTTACATAGCATTTATATTGTATTAGGTA	11294
QY	248	-----	248
Db	11295	GTATAGTATCTAGAGATGATTTAAAGAAATATCAGAGATGTGTAGTTATGCAAAAT	11354
QY	248	-----	248
Db	11355	ATTACCCCATTTTATTTATGTAAAGGATTTGAATATCTGTGGCTTTTGGTGTCTGTGGTG	11414
QY	249	-----Pro-----Ser-----	250
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QY	251	-----Ala-----GluPhe-----	253
Db	11475	TGCATGTGCTTTGTGTATGTCTTTTCTCCAGAGGTGAGAGTTCCTTACTTTCATCAG	11534
QY	254	-----Gln-----	254
Db	11535	ATTCTTAAAGAGAAATGTAGACCCAGAAAAAGTTAAAAACCATGGACCTAACAGGAATTTG	11594
QY	255	-----Trp-----Tyr-----	256
Db	11595	TTAAAGTGGAGCTAGAGGAAAACTGTAAAAAGTATTTGAAACAGTATCTGTGTCTTG	11654
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Db	11655	AATTAATGTTGGTTTCTCTCTTTATTTGTCGTAATGTGAATGAGTTTTCCTTTT	11714
QY	257	-----Lys-----	257
Db	11715	GAGAGATGATTTTCTACTTTAACTACTTAAGTTTCTTTATTTGTTGTTATGGTTTTC	11774
QY	258	-----Asp-----	259
Db	11775	TCCTTTTAAATTTGATTTATTTGAAGAACTCACATTAAAGATTATCAAAGTCTAGTTGCTTA	11834
QY	259	-----	259
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QY	260	-----Lys-----	260
Db	11895	GCAATATTTCCAGAGCAATAGATTTTTTTTATATATCACTTAAACGTGCTCAITTTATAG	11954
QY	261	-----Arg-----LeuIle-----	263
Db	11955	ATAAGAGGGTTAGTGCTGTATATTGACTTGTGTTAAAGTCATGTTGATTTCCAGTATATA	12014

Db	13095	ACACAGGGAATGTTACTGTGACTCTCTTCGGTTGGCAGTTGCTAAAGTCAACATTAATGGAAC	13155	:::
QY	300	-----Lys-----LeuGly-----His-----	303	
Db	13155	TTGATGAACATTCTCTACCCAGAAAGGATAACAATCTTGAATATACCACCTTTTGCGAGA	13214	
QY	304	-----Thr-----	304	Thr--
Db	13215	AGCTGTGACTTATGCTGTGGCATATAGGCCCTGGACTAAGAGTCAGTAGTTAGACTTC	13274	
QY	305	-----Asn-----	305	
Db	13275	TCITTTTGGTTGTCTTTTAATTCAGATCTGTGTAAATCTTTAGCTTTGCTTTATGCGCTT	13334	
QY	305	-----	305	
Db	13335	AGTTGTGTTTCACATATCCTCACAAAGATACAGATAACGTGATCTGTATCATTAAGTCTA	13394	
QY	306	-----Ala-----	307	Se
Db	13395	CAGGTTATTTATTTGGGGCCAGTCATGTGTGTGCAGCATAGAGTGGCAGTCAACAGTC	13454	
QY	307	r-----IleMet-----LeuPhe-----Gly-----	312	
Db	13455	AGTAGTAACCTGATGACTGCCACCACATAGTATACTCCCTTGTTTGTAGAGGTTCTCTATTA	13514	
QY	313	-----Pro-----	313	
Db	13515	TCTGAGTAGGGATATGAAGTGGTAGTTTCCCTTGCTCACTTAAGGACTCAAAAT	13574	
QY	313	-----	313	
Db	13575	TTTTCTGTCTGCTTAGGAAATATGACATCTTTTGTCTCTTTGCTCTGAGGGCAGTC	13634	
QY	313	-----	313	
Db	13635	GGAGAATTAAAGTAGTCTTTTATAAGBATGTGATGAATTTAGTGTAGTGTATATGTG	13694	
QY	314	Gly-----Ala-----Val-----SerGluVal-----SerAsnGlyThr--	323	
Db	13695	TTCAGGACTGAGAGCCTGGGTTATGCAAAGTCTGAGGTTTAGTTGACTAATGGTCACT	13754	
QY	324	-----Ser-----	324	
Db	13755	AGATTTAAATTAATTGGATGAATCAGTAGACTGGAAACCCCTTTGGCAAGCAGAGGTTGAA	13814	
QY	325	-----ArgArg-----Ala-----	327	
Db	13815	ACATCTTGGAAGATGAATAAACTAGCCTGGCAGATGAGACCAGGAGGATGAGTA	13874	
QY	327	-----	327	
Db	13875	CCAGTGTAAAGGAATATGTCTGTCTAGAGGGAACAGACAGTTAAGAAATTGAGAAACAGGCT	13934	
QY	328	Gly-----Cys-----	329	
Db	13935	GGCAAGGTGGCCACACCTGTATCCAGTGTTTTGGAGGCTGAGGTAGGAAGATCAC	13994	
QY	329	-----	329	
Db	13995	TTGAGGCCAGGAGTTCAATACCGAGCTGGGCAACATAGCGAGATCCCATCTTTATGAAA	14054	
QY	330	-----Val-----	330	
Db	14055	GTTAAAAAAGTAGCTGAGCGTGGTCATGAGTCTGTAGTCTCTAGCTTGGAGGCTGAC	14114	
QY	331	-Trp-----Leu-----Leu-----	334	Pr
Db	14115	ATGGGAGGATCGCTTGACCTAGAGTTTGAAGTTACAGTGAGCCATGAGTCACTGAGCC	14174	
QY	334	oLeu-----Leu-----	336	



Db 1315 GTAAGATAGACCTGTGTAGTACTAAGTCTCATATAAATAAAGCTATTACAAATATAT 1374  
QY 48 -----Arg-----  
Db 1375 TCCATCTCTAGGGAATGTTTTCTTAGGATTCGTGTAGCTGGTGGAAATCCCTATCTGT 1434  
QY 49 -----Gln-----  
Db 1435 TGGGTCTTAACAAGAGTAGAAGCTGGTCAGAAAGAGTGTATTCAGAGTAAGAGT 1494  
QY 50 -----Gly-----Glu-----SerAlaThr-----  
Db 1495 TTTGGGAAGACTACGATGAGTGTAGTATCTTAATCCAACTCCCAACTCCTCACTTGAAGGTGAA 1554  
QY 55 -----LeuArg-----Cys-----  
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QY 58 -----Thr-----  
Db 1615 GGAGTTAGTTACCTTGCAAAAGAGCCCATATGCCCTATCCCTACAAATCCCTCATTTGT 1674  
QY 59 -----Ile-----  
Db 1675 TCCAGGACACAGTTTGTAGTCAGATCCCGAGCATGTCCAGGGAGACAAATACAAAGTGTGA 1734  
QY 60 p-----AsnAr-----  
Db 1735 TCTGAAGAGCTCTTTTGTGATCTTAATATGTAGTGTGGAGATATCTGTGGAATAG 1794  
QY 62 g-----Val-----  
Db 1795 ATTCTGAATATAGGACCTTGGAGAAGAGACATAAATGGGTCAATGATCACTATGG 1854  
QY 64 -----Thr-----Arg-----Val-----  
Db 1855 GTAACCTATAGTAGAGATTTGGCTCAGTCTATGAGACTGAACAGCTTGAAGTAGTCT 1914  
QY 67 -----AlaTIPLeu-----  
Db 1915 TTTTACTGTGTGGAACACATTTTGACTCAGAGTGGCTCATCTAAATAGAGATGATAT 1974  
QY 70 -----Asn-----  
Db 1975 GCAGAAACTCCTGTGTATGATGATAGAGAAAGAAATCAAGAGAGGGGCCATGTTGG 2034  
QY 71 -Arg-----SerThr-----Ile-----  
Db 2035 GAGGATTTAATATGAGTGTATCTCTAACTGTATCCCTGTGTAAGAGTCTAGTCAACTCT 2094  
QY 75 uTyraLaGly-----  
Db 2095 TTACCAAGGCATTGAGAAAAACACTGGTGAGCAGACACCAGCACCTCTGAAAAGCCATA 2154  
QY 78 -----  
Db 2155 TAGTCTGTGTAGGCCAGAGATGCCAGTGGGAGATGCTTCAGTTGAATGGACCCCTTG 2214  
QY 78 -----  
Db 2215 ATTGATAGGCATTTTCAAGCTGTGCCATGTGTGAGAGACAAAGTAGTGATTTAATTTGCT 2274  
QY 79 -----Asn-----  
Db 2275 AGACTAGAAAGGTGGGATGTTCTCTGTAATAGACAGCAGGACACAGGATTAATCAGTA 2334  
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QY 82 p-----Cys-----LeuAspPro-----  
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QY 122 His-----Pro-----LysThrSer----- 126  
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QY 163 -----Pro-----Glu----- 164  
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Db 4792 AGCCACTTGTCTGCTTTGTGTCATCTCACTGACATTTCAACTCTTTTCAGTTACTGTATCTT 4851  
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LOCUS  
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genomic survey sequence.

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Pan troglodytes LRP1 gene, VIRTUAL TRANSCRIPT, partial sequence,  
genomic survey sequence.



ACCESSION AY404419  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE 1 (bases 1 to 12485)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios  
 JOURNAL Science 302 (5652), 1960-1963 (2003)  
 PUBMED 14671302  
 REFERENCE 2 (bases 1 to 12485)  
 AUTHORS Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA  
 COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.  
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 Best Local Similarity: 8.66% Mismatches: 4  
 Query Match: 69.17% Indels: 3035  
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 QY 6 -----ProLysMet-----His----- 9  
 Db 100 GATCTGACGAGGCC---CTGAGATTGTCCACAGAGTAAGGCCCGCAGCGATGCCCGGA 156  
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Db 1956 CGGCGTGGCGGCTGGAGAGGCGTGGATGGCTCACACCGAGACATCTTTGTCCACC 2015  
QY 79 -----Asn-----Asp-----Lys----- 81  
Db 2016 TCCAGACAGTCTTTGGCCCAATGGGCTAAGCTTGGACATCCAGCTGGGGCGCTCTAC 2075  
QY 82 Trp----- 82  
Db 2076 TGGTGGATGCTTCTACGCGCATCGAGACGATGCTCTCAATGGCACAGACCGGAAG 2135  
QY 83 -----Cys----- 83  
Db 2136 ATTGTGTATGAAGTCTCTGAGCTGAACACCGCTTTGGCCGTGTGTCCATGGCACTAC 2195  
QY 84 -----LeuAsp----- 85  
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QY 86 -----Pro-----Arg-----Val-----Val-----Leu 90  
Db 2256 GGNNNCCCACTGTGACCCCTTCTGGCGAGTGGAGCGGCCCCCATCTTTGAGATCCGAATG 2315  
QY 91 Leu-----SerAsn----- 93  
Db 2316 TATGATGCCAGCAGCAAGTGGCACCAACAAATGCCGGGTGAACAATGGCGGTGC 2375  
QY 94 -----Thr-----Gln-----Thr-----Gln----- 97  
Db 2376 AGCAGCTGTGTGGCCACCCCTGGAGCGCCGAGTGGCGCTGTGTCTGAGGACCAAGTG 2435  
QY 98 -----TyrSerIle----- 100  
Db 2436 TTGACGACAGCGGCTCACTGTGTGGCGAACCCATCTCTAC---GTGCTCCACCCCGAG 2492  
QY 101 -----Glu-----IleGln----- 103  
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QY 104 -----Asn-----ValAsp----- 106  
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QY 107 -----Val-----Tyr----- 108

Db 2613 ACCTGCCCTCGGACCGGATTCAAGTGGAGAACCAACCGGTGCATCCCAACCGCTGGCTC 2672  
QY 109 -----AspGlu----- 110  
Db 2673 TGGACGGGACAAATGACTGTGGGACAGTGAAGATGAGTCAATGCCACTTGTTCNNCC 2732  
QY 111 -----Gly-----Pro-----Tyr 113  
Db 2733 CGCACTGCCCGCCCAACACAGTTCCTGTGTCAGTGGCCGCTGCATCCCATCTCTGG 2792  
QY 114 ThrCys-----Ser----- 116  
Db 2793 ACGTGTGATCTGGATGACGACTGTGGGACCGCTCTGTATGAGTGTGTCTGTGTGCTTAT 2852  
QY 117 -----ValGln-----Thr----- 119  
Db 2853 CCCACTGTCTCCCGCTGACTCAGTTTACCTTGCACAAATGGCAGATGTATCAACATCAAC 2912  
QY 120 -----AspAsn-----His 122  
Db 2913 TGGAGATGCGACAATGNNNNNNNNNGTGGGACAAACAGTGCAGGAAGCGGCTGCAGCCAC 2972  
QY 123 -----ProLys-----Thr 125  
Db 2973 TCCTGTTNAGACCCAGTTCAAGTGCAACAGCGGGCTTGCATCCCGAGCACTGGACC 3032  
QY 126 -----Ser----- 126  
Db 3033 TGGATGGGACAATGACTGCGGAGACTACAGTGTATGAGACACACGCAACTGCACCAAC 3092  
QY 127 -----Arg-----ValHis----- 129  
Db 3093 CAGGCCACGAGGCCCCCTGGTGGCTGCACACATGATGAGTTCAGTGCAGTCCGCTGGATGA 3152  
QY 130 Leu-----ValGln----- 133  
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QY 134 -----ValSer-----Pro-----Lys 137  
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QY 138 -----Ile-----Val-----Glu 140  
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QY 146 -----SerIle-----Asn----- 148  
Db 3390 GCCAACAAACCTCAGTCTCCCTGCGCTGACAAAGCTGTGTATGGCAACAGCACTGT 3449  
QY 149 -----GluGly-----AsnAsn----- 152  
Db 3450 GGGACGGCTCAGATGAGGGGAGAGCTTGGCAGCAGTGTCTCTGAATAACGGTGGCTGC 3509  
QY 153 -----Ile-----Ser----- 154  
Db 3510 AGCCACAACCTCAGTGGCACCTGGCGAAGGATTTGTGTCTCTGCTCCCTCTGGGCATG 3569  
QY 155 -----Leu-----ThrCys-----Ile-----Ala----- 159  
Db 3570 GAGCTGGGGCCCGACACACACCTGCGAGATCCAGAGCTACTGTGTGCCAAGCATCTCAA 3629  
QY 160 -----Thr----- 160  
Db 3630 TGCAGCAAAAGTGGCGACAGAACAGTTCAGCGTGAAGTGTCTCTGTCTACGAGGGCTGG 3689  
QY 161 -----Gly-----Arg-----Pro----- 163

Db 3690 GTCTGGAACCTGACGGCAGAGGTGCCGAGCGCTGGNCCCTTCAAGCGCTTCATCAT 3749  
QY 164 -----Glu----- 164  
Db 3750 TTCTCCAACGCCATGAATCCGGCGCATCGATCTTCAAAAGAGACTACAGCGCTCTG 3809  
QY 165 ---Pro----- 165  
Db 3810 GTGCCCGGCTGCGCAACACCATCGCCCTGGAATTCCACCTCAGCAGCGCCCTCTAC 3869  
QY 165 ----- 165  
Db 3870 TGCACCGACGTGTGGAGGCAAGATCTACCGGGGAAGCTGCTGGACACGAGCGCTG 3929  
QY 166 Thr-----Val----- 168  
Db 3930 ACTAGTTTCAGGTGTGATTCAATGAGTGGCTGGCCACCCAGAGGCCTAGCTGAGNC 3989  
QY 169 -----Trp----- 169  
Db 3990 TGGATTGCAGGCATCTACTGGTGGAGAGTAACCTGGATCAGATCGAGGTGGCCAAG 4049  
QY 170 -----Arg-----His----- 171  
Db 4050 CTGGATGGGACCTCCGGACCAACCTGCTGGCCGGTGACATTCAGCACCCAGGGCAATC 4109  
QY 171 ----- 171  
Db 4110 GCACTGGATCCCGGATGGATCTCTTTTGGACAGACTGGGATGCCAGCTGCCCGC 4169  
QY 172 Ile-----Ser 173  
Db 4170 ATTGAGCAGCCTCCATGAGTGGGCTGGCGCGCACCGTGCCACCGGGAGACCGCTCT 4229  
QY 174 -----Pro-----Lys----- 175  
Db 4230 GGGGGTGGCCCAACGGGCTACCGTGGACTACCTGGAGAAGGCATCTCTTGGATTGAC 4289  
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QY 184 -----Glu----- 184  
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QY 186 -----Leu-----Glu 187  
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Db 4770 GACATCGAACAGCTCACTAGTGTAGACTAGGATGCCCGGAGCGGTGTGTACTGGTCT 4829

QY 195 ----- 195  
Db 4830 GAGTCGGGACACAGGCCATCAAGCGGCTTTCATCAACGGCACAGGAGTGGAGACAGTC 4889  
QY 196 ---Ser----- 196  
Db 4890 GTCTCTGAGNN 4949  
QY 196 ----- 196  
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QY 196 ----- 196  
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QY 197 -----GlyAsp----- 198  
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QY 198 ----- 198  
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QY 199 -----Tyr----- 199  
Db 5190 GAAAGCAACTCTACTGGATCAGCTCCGGGAACCATACCATCAACCGCTGCAACCTGGT 5249  
QY 199 ----- 199  
Db 5250 GGGNN 5309  
QY 200 -----Glu-----Cys 201  
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Db 5490 AACAAAGGTGACTGCTCCNNNNNNNGCCTGCCACGTCAGAGACGACCGCTCTGTCATG 5549  
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QY 209 ---Ala-----ProVal----- 211  
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QY 212 -----Val----- 212  
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QY 213 -----Arg-----ArgValLys-----Val 217  
Db 5790 CAGACGTGGGTGAAGACGTGTGTGACCAATGGCAATGGCCGTGGGGGCAATTCAGTGT 5849  
QY 218 -----Thr-----Val----- 219  
Db 5850 GACTGGATCGCAGGCAACATCTACTGGACAGACGAGGCTTTGATGTATCGAGGTCCGC 5909

Qy	220	----	Asn	----	Tyr	----	Pro	----	222
Db	5910	CGCTCAATGGCTCTTCCGCTACGTGTGTGATCTCCAGGGTCTAGACAAGCCCGGGCC	5969						
Qy	223	----	Pro	----	Tyr	----	Tyr	----	224
Db	5970	ATCACCGTCCACCCGGAGAAAGGGTACTTGTCTGGACTGAGTGGGTCAGTATCCAGT	6029						
Qy	225	Ile	Ser	----	Glu	----			227
Db	6030	ATTGAGCGGTCTCGGCTNNNTGGCACGAGCGTGTGGTGTGCTCAACGTCAAGTCAGCATCAGC	6089						
Qy	228	----					Ala	----	228
Db	6090	TGGCCCAACGGCATCTCAGTGGACTACGAGATGGGAAGCTGTAAGTTCATCTACTGGAGTCACGG	6149						
Qy	229	----	Lys	----	Gly	----			230
Db	6150	ACAGACAAGATTGAACGGATCGACTGGAGACGGGTGAGAACCAGAGGTGGTCTCTGTC	6209						
Qy	230	----							230
Db	6210	AGCAACAATGGAATGTTTTCAGTGTCTGTGTGTTGAGGATTTCAATCTACTGGAGTCAC	6269						
Qy	231	----	Thr	----	Gly	----	Val	----	233
Db	6270	AGGACTCATGCCAACGGCTCTATCAAGCGCGGGAGCAAGACAATGCCAGACTCCGTG	6329						
Qy	234	Pro	ValGly	----					236
Db	6330	CCCCTGGAACCGGCATCGGCGTCCAGCTTAAAGACATCAAAGTCTTCAACGGGACCGG	6389						
Qy	237	GlnLysGlyThr					Leu	----	241
Db	6390	CAGAAAGCCACCAACGNTGGCGGTGGCCAATGGCGGGTCCAGCAGCTGTGCTGTAC	6449						
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Db	6450	CGGGCCGTGGGCAGCGGGCTGTGGCTGTGCTCACGGATGTGGTGAAGACGAGCA	6509						
Qy	246	Ser							246
Db	6510	TCGTGCCGATATGCCGCTACCTCTCTACTCAGAGCGCAACATTTCAAGATATC	6569						
Qy	247	----	Ala	Val	----	ProSerAla			251
Db	6570	CACGTGCGGATGAGCGCAACCTCAATGCGCGCGTGCAGCCCTTCGAGGACCT	6623						
Qy	252	Glu							252
Db	6624	GAGCACATGAAGACGTCATCGCCCTGGCTTGAATAACGGGAGGCCTCTCCGGGC	6683						
Qy	253	----	Phe	----	Gln	----			254
Db	6684	ACCCCAATCGCATCTTCTTACGCGACATCCACTTTGGGAACATCCAAACAGATCAACGAC	6743						
Qy	254	----							254
Db	6744	GATGGCTCCAGGAGGATCACCATTTGTGAAAAAGTGGGCTCGGTGGAAGCCCTGCGCTAT	6803						
Qy	255	----	Trp	Tyr	----				256
Db	6804	CACCGTGGCTGGGACACTCTGTATTGGACAANCTACACGACATCCACCATCAGCGCCAC	6863						
Qy	257	----				Lys	----		257
Db	6864	ACAGTGACCAACCCCGCCAGGGGCTTCGAGCGTGAGACCGTCACTATGTCTGGA	6923						
Qy	258	AspAsp							259
Db	6924	GATGACACCCACGGGCTTTGTTTGGACGAGTGCAGANNNNNNNNNNNNNNNNNN	6983						
Qy	259	----							259

[illegible]

Db	8064	TACTGGACAGATGTGACGAGCCAGGGCGAGCATGATCCGAAGGATGCACCTTAAOCCGGAGC	8123
Qy	294	-----	294
Db	8124	AATGTGCAGGTCTCTACACGGTACAGGCGCTNNNCACCCGATGGGCTGGCTGGTGGACTGG	8183
Qy	295	-----Cys-----Val-----	296
Db	8184	GTGGGTGCAACCTGTACTGTGGTGCACAAAGCGCCGAGACACCATCATGAGTGTCCCAAGCTC	8243
Qy	297	-----Ala-----Ser-----	298
Db	8244	AATGGGGCTTATTCGGAACGGTGTGGTTCAGCTCTGGCCCTCCGTGAGCCAGGGCTCTGGTG	8303
Qy	299	-----Asn-----	299
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Qy	300	-----Lys-----	300
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Qy	300	-----	300
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Qy	303	-----His-----Thr	304
Db	8544	CCGCACATCTTTTGCACTGACCTGTTTGAGGACTACGTCTACTGGACCGACTGGGAAACA	8603
Qy	305	-----Asn---Ala-----Ser---Ile-----	308
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Qy	309	-----Met---Leu---Phe-----	311
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Qy	312	-----Gly-----ProGly-----	314
Db	8724	CACCCCTGCAAGTCAACAATGTGGTGCAGCAACCTGTGCCTGTGTCCCCCGGGGGA	8783
Qy	315	-----Ala-----Val	316
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Qy	317	Ser-----	317
Db	8844	TCCAACTGCACGGCTAGNN	8903
Qy	317	-----	317
Db	8904	NN	8963
Qy	317	-----	317
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Qy	318	-----Glu-----	318
Db	9024	ATCTGCGATGGGACAAATGACTGCCAGGACAAAGTGCAGGGCAACTGTGATCCAC	9083
Qy	319	Val-----Ser-----	320
Db	9084	GTCTGTCTTGCACAGTCACTGTTCAAATGCACCAACCAACCGCTGATTCCCGGCATCTTC	9143
Qy	321	-----AsnGly-----	322
Db	9144	CGTGCATATGGCGAGGCAAACTGGGAGATGGGAGGATGAGAGGAGCTGCCNNNNNTTG	9203

QY	322	-----	322	
Db	9204	ACCTGGCCCCCAACCAAGTTCAGTGTCTCATTTACCAACGGTGCATCCCGCGGTCGG	9263	
QY	322	-----	322	
Db	9264	GTCCTGGACCGGGAACAATGACTGTGTGGATGGCAGTGAAGCGCCGCAACTGCACCCAG	9323	
QY	323	-----	323	
Db	9324	ATGACCTGTGTGTGCGACGAGTTCGGCTGCAAGGATTCGGCGCGCTGCATCCAGCGCGT	9383	
QY	324	-----	324	
Db	9384	TGGAAGTGTGACGAGAGGATGACTGTGGGATGGCTCGGATGAGCCCAAGGAAGAGTGT	9443	
QY	324	-----	324	
Db	9444	GNNN	9503	
QY	324	-----	324	
Db	9504	NN	9563	
QY	325	---Arg-----	328	
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QY	328	-----	328	
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QY	329	-----	331	
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QY	331	-----	331	
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QY	338	-----	338	
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QY	339	-----	340	
Db	10044	GAGCCCCCAGCCAGCCACCACTGCAAGACAAGAGGAGTTCTGTGCCGGAAC	10103	
QY	341	-----	344	
Db	10104	CAGCGCTGCCTCTCCTCTCCTCGCGCTGCAACATGTTTC	10142	
RESULT	29			
LOCUS	AY405011			
DEFINITION	Mus musculus HCM2081 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.	9567 bp	DNA	linear
ACCESSION	AY405011			
VERSION	AY405011.1			
KEYWORDS	GSS			

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SOURCE      Mus musculus (house mouse)
ORGANISM    Mus musculus
REFERENCE    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 9567)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE       Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL     Gene trios
PUBMED      Science 302 (5652), 1960-1963 (2003)
REFERENCE    14671302
AUTHORS      Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferreira,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
COMMENT      Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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             /mol_type="genomic DNA"
             /db_xref="taxon:10090"
             <1..>9567
             /locus_tag="HGM2091"
gene         us-10-017-084a-523 (1-344) x AY405011 (1-9567)
ORIGIN
Alignment Scores:
Pred. No.:      1..11e-12      Length:      9567
Score:          1665.50      Matches:    283
Percent Similarity: 11.03%      Conservative: 48
Best Local Similarity: 9.43%      Mismatches: 6
Query Match:    69.17%      Indels:     2666
DB:             29          Gaps:        248

US-10-017-084A-523 (1-344) x AY405011 (1-9567)

Qy      1 MetLys-----Thr-----Ile----- 4
Db      373 ATGGAAGAGTTTCCTCTCCCCACCTGATGTTGTTCAGACACCAATGGATGCACGCA 432
Qy      5 -----Gln-----ProLys-----Met----- 8
Db      433 TTTTCCAGTCCCTGGAATTCGCCAGCCCTCTAGAGACTGCCAATGCCCAAGATTTA 492
Qy      9 -----His----- 9
Db      493 TACTCCAGCAAGAAATTATATGAATTAACCGTTTATATAGCATATCCATCCAGAG 552
Qy      9 ----- 9
Db      553 TTAAGAAAACTTAGAAAAAGATTACATCAGTGAGGTTCTGAAATGTTTCTAGCCAG 612
Qy      9 ----- 9
Db      613 ATAACTCAGGAACGGCTTATCAGCATGTACAAAAGCTCGTATGTTTTCGAAAT 672
Qy      10 -----AsnSer----- 11
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Qy      12 Ile-----Ser-----Trp----- 14
Db      733 ATCTCAAGAGAGGTGCGATTCGATTCGATGGATTTTGTGAAATCAGCCATTAGATTCT 792
Qy      15 -----Ala----- 15
Db      793 ATCAACCATGGTTCTACAGATGAAGGTGACACTTCCAAAGGCATTTGTGACCAAGAACTA 852

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Qy      18 -----Thr-----Gly-----LeuAla----- 21
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Qy      22 -----Ala-----Leu----- 23
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Qy      27 -----Gln-----Gly----- 28
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Db      1513 CTGAAACACAGACAGTCATAGGTACAGATGTTTCTTAAAGAGTG-TTGGATGTTTGAAC 1571
Qy      45 -----Val-----ValThr----- 46
Db      1572 ACAGCCATTAGACATTCTAAAGACTCTCTGTATACGACAGTGTATCATCTGAGAGAG 1631
Qy      47 -----Val----- 47
Db      1632 AATAGAGGTGATGTAAAGACCACCAACATCTATTGTGAACACTCCCAATAGAGGCTTT 1691
Qy      48 -----ArgGln----- 49
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Qy      50 -----Gly----- 50
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Qy      51 -----Glu-----Ser-----Ala-----Thr----- 54
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QY 75 -----LeuTyr----- 76  
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QY 77 -----Ala----- 77  
Db 2712 AGCCGAGACATTCAGAAAGGCAATGTTCTAAATGCGAGTGGCTATTGTAACCAACCC 2771  
QY 78 -----Gly---Asn---Asp----- 80  
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QY 81 ---LysTrp---Cys-----Leu-----Asp 85  
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QY 85 ----- 85  
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QY 86 -----Pro 86  
Db 2952 TGATGTGAAAGCTACAAAATGCTTTTGAACACAAACCCTCTATGCAATTCAGACCA 3011  
QY 87 ---ArgVal----- 88

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QY 94 ----- 94  
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LOCUS
DEFINITION
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genomic survey sequence.
ACCESSION
AY404089.1
VERSION
AY404089.1
KEYWORDS
GSS.
SOURCE
Pan troglodytes (chimpanzee)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE
AUTHORS
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 11490)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL
Science 302 (5652), 1960-1963 (2003)
PUBMED
14671302
REFERENCE
AUTHORS
2 (bases 1 to 11490)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE
Direct Submission
JOURNAL
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Best Local Similarity: 10.05% Mismatches: 11
Query Match: 69.05% Indels: 2434
DB: 239
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Qy 7 ---Lys----- 7
Db 99 GAAAAATCTTTATATACATTTTTCAGAGGATTTGACTTTATTGATGAGATGCCACTTAT 158
Qy 8 -----Met-----His-----AsnSer 11
Db 159 CCCAGAACTATACATAGAGAGGTGACATGTGTGGAACTCATTAGACTCAGGATGCC 218
Qy 12 Ile-----Ser----- 13
Db 219 ATCGTTAGTCATTTTAGACGATGAATCTGAAGACACAGCTTCCAGAAATTTTAGCAGACAT 278
Qy 14 -----Trp-----Ala 15
Db 279 TGTACAAAACCTTGGAGGGTTTGTCTTAAATAATTAGATGCATCTATATACATCCGCT 338
Qy 16 -----Ile-----PheThr-----Gly----- 19
Db 339 TATTAAAAATATATTTCATTCACCATTCACCAAGTGTGTTTGCAGNATATGAGAGAT 398
Qy 20 ---LeuAla-----AlaLeu-----Cys--- 24
Db 399 GCCATTGCAGAAATTTGTGAATGAATAAATCTGCTACTTCCCAACACACAAAGATGCCCT 458
Qy 25 -----Leu-----Phe-----Gln----- 27
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Qy 28 ---Gly----- 28
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Qy 59 -----Ile-----Asp-----Asn----- 61
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Db 1224 AGCCTGAAGAAAGCCCTCAAAATATCCAGGCTCTTTGGTCTGGAAGAGATCTCTG 1283
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Qy 78 y-----Asn-----Asp-----Lys----- 81
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Qy 102 -----Ile-----Gln----- 103
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Qy 105 -----ValAsp----- 106
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Qy 114 -----Thr-----CysSer--- 116
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QY 310 -----Leu----- 310
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